

```

; Sequence 5863, Application US/09960352
; Patent No. US20020137139a1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing

```

APPLICANT: Bvatt, John C.
APPLICANT: Mathiasagan, Nagappan
TITLE OF INVENTION: NOCTIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: MUSCLE AND FAT DEPOSITION
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5863
LENGTH: 424
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 25-LIB34-026-Q1-EL-G1
US-09-960-352-5863

Query Match 54.0%; Score 54; DB 10; Length 424;
Best Local Similarity 76.7%; Pred. No. 6e-09;
Matches 66; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 14 CACAGGAGCTGTGACCTGGACAAAGGGGAGTGTGACCACTTGTGCGGAGGAGACA 73
b 11 CACCGGTGACATCTGCACCTGGACCAATGGGGCTGCCACCAAGTTCTGACGAGGAGCG 70

QY 74 GAACCTGTGTGTGCTCTGCGCCG 99
Db 71 CAGCGAGGTGGGTCTCTCTGCGCG 96

RESULT 3
US-09-867-701-3188/c
Sequence 3188, Application US/09867701
Patent No. US20020132237A1
GENERAL INFORMATION:
APPLICANT: Ajiata, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.497
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3188
LENGTH: 295
TYPE: DNA
ORGANISM: Homo sapien
US-09-867-701-3188

Query Match 30.8%; Score 30.8; DB 10; Length 295;
Best Local Similarity 63.5%; Pred. No. 0.24;
Matches 47; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 27 TGCAGCTGGACAAAGGGGAGTGTGACCACTTGTGCGGAGGAGACAAGACTGTGTG 86
Db 108 TGCAGCGAGGAGAAAGGGGCTGCTCCAGATCTGCCAACAAGCGGGTACTTCCAC 49

QY 87 TGTCTGTGCGCCG 100
Db 48 TGTCTGTGCGACAG 35

RESULT 4
US-10-044-090-780
Sequence 780, Application US/10044090
Patent No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850

SOFTWARE: PERL Program
SEQ ID NO 780
LENGTH: 7132
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 198499.13
US-10-044-090-780

Query Match 29.6%; Score 29.6; DB 12; Length 7132;
Best Local Similarity 61.8%; Pred. No. 1.4;
Matches 47; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 20 GAACCTGTGACCTGGACAAAGGGGAGTGTGACCACTTGTGCGGAGGAGACAAGACTC 79
Db 78 GGAACAATGCAATCTTAAACAAGGTGCTGTGCCCAAGAGTCCAGATGCTGCGGGCGC 137

QY 80 TGTGTGTGCTCTGCG 95
Db 138 AGTCCACTGTACTGCG 153

RESULT 5
US-10-001-189-40/c
Sequence 40, Application US/10001189
Patent No. US20020173634A1
GENERAL INFORMATION:
APPLICANT: FRASER JR., MALCOLM J.
APPLICANT: LI, XU
APPLICANT: BEAM, TERESA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSPOSITION USING
TITLE OF INVENTION: MINIMAL SEGMENTS OF THE EUKARYOTIC TRANSFORMATION
FILE REFERENCE: 835910-92098
CURRENT FILING DATE: 2001-10-30
PRIORITY FILING DATE: 2000-11-01
PRIORITY FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 40
LENGTH: 707
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ITR Cartridge
US-10-001-189-40

Query Match 28.2%; Score 28.2; DB 9; Length 707;
Best Local Similarity 61.6%; Pred. No. 2.2;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 18 CGAAGCTCTGCAAGCTGTGACAAAGGGGAGTGTGACCACTTGTGCCAGGAGAGACAAG 77
Db 358 CTGATCGGCTTGGGCTGACCAATCGGAACCTGTGTCCGAAAAGCCGCGCAACTGTGA 299

QY 78 TGTGTGTGTGTGT 90
Db 298 TCCAGAGTGGCGT 286

RESULT 6
US-10-001-189-41/c
Sequence 41, Application US/10001189
Patent No. US20020173634A1
GENERAL INFORMATION:
APPLICANT: FRASER JR., MALCOLM J.
APPLICANT: LI, XU
APPLICANT: BEAM, TERESA

;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSPOSITION USING
;; TITLE OF INVENTION: MINIMAL SEGMENTS OF THE EUKARYOTIC TRANSFORMATION
;; FILE REFERENCE: 835910-92098
;; CURRENT APPLICATION NUMBER: US/10/001,189
;; PRIOR FILING DATE: 2001-10-30
;; PRIOR APPLICATION NUMBER: 60/244,984
;; PRIOR FILING DATE: 2000-11-01
;; PRIOR APPLICATION NUMBER: 60/244,677
;; NUMBER OF SEQ ID NOS: 70
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 41
;; LENGTH: 3662
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: pXL-Bac
;; OTHER INFORMATION: sequence
S-10-001-189-41

Query Match 28.2%; Score 28.2; DB 9; Length 3662;
Best Local Similarity 61.6%; Pred. No. 3.5;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 18 CGGAAGCTCTGACGCTGACACGCGGACTGTGACCACTTCTGCCACGAGACAGAAC 77
DB 1339 CTGATGCGCTTGGGCTGACCATCCGGAACGTGTCTCCGAAAGCCCGACGAACCTGTA 1280
QY 78 TCTGTGCTGTGCT 90
DB 1279 TCCGAGGTGGCT 1267

RESULT 7
US-10-001-189-46/c
; Sequence 46, Application US/10001189
; Patent No. US20020173634A1
; GENERAL INFORMATION:
; APPLICANT: FRASER JR., MALCOLM J.
; APPLICANT: LI, XU
; APPLICANT: BEAM, TERESA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSPOSITION USING
; TITLE OF INVENTION: MINIMAL SEGMENTS OF THE EUKARYOTIC TRANSFORMATION
; FILE REFERENCE: 835910-92098
; CURRENT APPLICATION NUMBER: US/10/001,189
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,984
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/244,677
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 4613
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pCR11-TTR
; OTHER INFORMATION: sequence
; NAME/KEY: CDS
; LOCATION: (344)..(922)
US-10-001-189-46

Query Match 28.2%; Score 28.2; DB 9; Length 4613;
Best Local Similarity 61.6%; Pred. No. 3.7;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 18 CGGAAGCTCTGACGCTGACACGCGGACTGTGACCACTTCTGCCACGAGACAGAAC 77
DB 651 CTGATGCGCTTGGGCTGACCATCCGGAACGTGTCTCCGAAAGCCCGACGAACCTGTA 592

QY 78 TCTGTGCTGTGCT 90
DB 591 TCCGAGGTGGCT 579

RESULT 8
US-10-001-189-53
; Sequence 53, Application US/10001189
; Patent No. US20020173634A1
; GENERAL INFORMATION:
; APPLICANT: FRASER JR., MALCOLM J.
; APPLICANT: LI, XU
; APPLICANT: BEAM, TERESA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSPOSITION USING
; TITLE OF INVENTION: MINIMAL SEGMENTS OF THE EUKARYOTIC TRANSFORMATION
; FILE REFERENCE: 835910-92098
; CURRENT APPLICATION NUMBER: US/10/001,189
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,984
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/244,677
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 4941
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pXL-Bac-ECFP
; OTHER INFORMATION: sequence
US-10-001-189-53

Query Match 28.2%; Score 28.2; DB 9; Length 4941;
Best Local Similarity 61.6%; Pred. No. 3.8;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 18 CGGAAGCTCTGACGCTGACACGCGGACTGTGACCACTTCTGCCACGAGACAGAAC 77
DB 778 CTGATGCGCTTGGGCTGACCATCCGGAACGTGTCTCCGAAAGCCCGACGAACCTGTA 837
QY 78 TCTGTGCTGTGCT 90
DB 838 TCCGAGGTGGCT 850

RESULT 9
US-10-001-189-54/c
; Sequence 54, Application US/10001189
; Patent No. US20020173634A1
; GENERAL INFORMATION:
; APPLICANT: FRASER JR., MALCOLM J.
; APPLICANT: LI, XU
; APPLICANT: BEAM, TERESA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSPOSITION USING
; TITLE OF INVENTION: MINIMAL SEGMENTS OF THE EUKARYOTIC TRANSFORMATION
; FILE REFERENCE: 835910-92098
; CURRENT APPLICATION NUMBER: US/10/001,189
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,984
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/244,677
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 4943
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: PBS-ITR-ECFP
OTHER INFORMATION: sequence
US-10-001-189-54

Query Match
Best Local Similarity 28.2%; Score 28.2; DB 9; Length 4943;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 18 CGGAAGCTCTGACCTTGACGACGAGGAGCTGTGACCACTTCCGACGAGACGAGAAC 77
DB 1076 CTGATGCCCTTCGGCTCGACCATCCGAACTGTCCGAAAACCCCGACGAACTGTGTA 1017
QY 78 TCTGTGTGTGCT 90
DB 1016 TCCAGGTGGCT 1004

RESULT 10
US-10-001-189-55/c
Sequence 55, Application US/10001189
Patent No. US20020173634A1
GENERAL INFORMATION:
APPLICANT: FRASER JR., MALCOLM J.
APPLICANT: LI, XU
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSCRIPTION USING
TITLE OF INVENTION: MINIMAL SEGMENTS OF THE EUKARYOTIC TRANSCRIPTION
FILE REFERENCE: 835910-92098
CURRENT APPLICATION NUMBER: US/10/001,189
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/244,984
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/244,677
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentlin Ver. 2.1
SEQ ID NO 55
LENGTH: 4944
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PBS-ITR-EGFP
US-10-001-189-55

Query Match
Best Local Similarity 28.2%; Score 28.2; DB 9; Length 4944;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 18 CGGAAGCTCTGACCTTGACGACGAGGAGCTGTGACCACTTCCGACGAGACGAGAAC 77
DB 1076 CTGATGCCCTTCGGCTCGACCATCCGAACTGTCCGAAAACCCCGACGAACTGTGTA 1017
QY 78 TCTGTGTGTGCT 90
DB 1016 TCCAGGTGGCT 1004

RESULT 11
US-10-001-189-56/c
Sequence 56, Application US/10001189
Patent No. US20020173634A1
GENERAL INFORMATION:
APPLICANT: FRASER JR., MALCOLM J.
APPLICANT: LI, XU
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSCRIPTION USING
TITLE OF INVENTION: MINIMAL SEGMENTS OF THE EUKARYOTIC TRANSCRIPTION
FILE REFERENCE: 835910-92098
CURRENT APPLICATION NUMBER: US/10/001,189
CURRENT FILING DATE: 2001-10-30

PRIOR APPLICATION NUMBER: 60/244,984
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/244,677
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentlin Ver. 2.1
SEQ ID NO 56
LENGTH: 4944
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PBS-ITR-EYFP
US-10-001-189-56

Query Match
Best Local Similarity 28.2%; Score 28.2; DB 9; Length 4944;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 18 CGGAAGCTCTGACCTTGACGACGAGGAGCTGTGACCACTTCCGACGAGACGAGAAC 77
DB 1076 CTGATGCCCTTCGGCTCGACCATCCGAACTGTGTCCGAAAACCCCGACGAACTGTGTA 1017
QY 78 TCTGTGTGTGCT 90
DB 1016 TCCAGGTGGCT 1004

RESULT 12
US-10-001-189-51
Sequence 51, Application US/10001189
Patent No. US20020173634A1
GENERAL INFORMATION:
APPLICANT: FRASER JR., MALCOLM J.
APPLICANT: LI, XU
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSCRIPTION USING
TITLE OF INVENTION: MINIMAL SEGMENTS OF THE EUKARYOTIC TRANSCRIPTION
FILE REFERENCE: 835910-92098
CURRENT APPLICATION NUMBER: US/10/001,189
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/244,984
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/244,677
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentlin Ver. 2.1
SEQ ID NO 51
LENGTH: 4951
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: pXL-Bac-EYFP
US-10-001-189-51

Query Match
Best Local Similarity 28.2%; Score 28.2; DB 9; Length 4951;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 18 CGGAAGCTCTGACCTTGACGACGAGGAGCTGTGACCACTTCCGACGAGACGAGAAC 77
DB 778 CTGATGCCCTTCGGCTCGACCATCCGAACTGTGTCCGAAAACCCCGACGAACTGTGTA 837
QY 78 TCTGTGTGTGCT 90
DB 838 TCCAGGTGGCT 850

RESULT 13
US-10-001-189-52
Sequence 52, Application US/10001189

```
Patent No. US20020173634A1
GENERAL INFORMATION:
APPLICANT: FRASER JR., MALCOLM J.
APPLICANT: LI, XU
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSPOSITION USING
TITLE OF INVENTION: MINIMAL SEGMENTS OF THE EUKARYOTIC TRANSFORMATION
FILE REFERENCE: 835910-92098
CURRENT APPLICATION NUMBER: US/10/001,189
PRIOR FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/244,984
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/244,677
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 52
LENGTH: 4952
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: pXL-Bac-Egfp
US-10-001-189-52

Query Match
Best Local Similarity 28.2%; Score 28.2; DB 9; Length 4952;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 18 CGAAGCTCTGCACCTGCAGCAACGGGAGCTGTGACCATCTTCCGACGAGCAAGAAC 77
DB 778 CTGATGCGCTCGGCTCGGACCATCCGGAAGTGTCTCGGAAAGCCGACGAACTGTGTA 837
QY 78 TCTGTGTGTGCT 90
DB 838 TCCCACTGCGCT 850

RESULT 14
US-10-001-189-48
Sequence 48, Application US/10001189
Patent No. US20020173634A1
GENERAL INFORMATION:
APPLICANT: FRASER JR., MALCOLM J.
APPLICANT: LI, XU
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSPOSITION USING
TITLE OF INVENTION: MINIMAL SEGMENTS OF THE EUKARYOTIC TRANSFORMATION
FILE REFERENCE: 835910-92098
CURRENT APPLICATION NUMBER: US/10/001,189
PRIOR FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/244,984
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/244,677
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 48
LENGTH: 8999
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: p(PZ)-Bac-Eyfp
US-10-001-189-48

Query Match
Best Local Similarity 28.2%; Score 28.2; DB 9; Length 8999;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 18 CGAAGCTCTGCACCTGCAGCAACGGGAGCTGTGACCATCTTCCGACGAGCAAGAAC 77
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DB 8593 CTGATGCGCTTCCGCTGCAGCATCCGAACTGTCTCGGAAAGCCGACGAACTGTGTA 8652
QY 78 TCTGTGTGTGCT 90
DB 8653 TCCCACTGCGCT 8665

RESULT 15
US-10-001-189-49
Sequence 49, Application US/10001189
Patent No. US20020173634A1
GENERAL INFORMATION:
APPLICANT: FRASER JR., MALCOLM J.
APPLICANT: LI, XU
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSPOSITION USING
TITLE OF INVENTION: MINIMAL SEGMENTS OF THE EUKARYOTIC TRANSFORMATION
FILE REFERENCE: 835910-92098
CURRENT APPLICATION NUMBER: US/10/001,189
PRIOR FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/244,984
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/244,677
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 49
LENGTH: 9012
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: p(PZ)-Bac-EcFP
US-10-001-189-49

Query Match
Best Local Similarity 28.2%; Score 28.2; DB 9; Length 9012;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 18 CGAAGCTCTGCACCTGCAGCAACGGGAGCTGTGACCATCTTCCGACGAGCAAGAAC 77
DB 8606 CTGATGCGCTTCCGCTGCAGCATCCGAACTGTCTCGGAAAGCCGACGAACTGTGTA 8665
QY 78 TCTGTGTGTGCT 90
DB 8666 TCCCACTGCGCT 8678

Search completed: January 15, 2003, 22:32:21
Job time : 36.5 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2003, 19:39:40 : Search time 1268 Seconds
(without alignments)
1277.247 Million cell updates/sec

Title: L00394_COPY_1_100
Perfect score: 100
Sequence: 1 CTCCTTTGGCAGTCACACGCG.....GTGGTGTGCTCTGCGCCCG 100

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estdb:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
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12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_iny:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_trod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	88.4	88.4	407	12	BE839155 RC6-FN013
2	88.4	88.4	716	13	B1757668 603028107
3	88.4	88.4	844	9	AL553470 AL553470
4	88.4	88.4	882	14	B0882177 ACENCOURT
5	88.4	88.4	898	9	AL521984 AL521984
6	88.4	88.4	984	9	AL570383 AL570383

Result No.	Score	Query Match	Length DB	ID	Description
7	88.4	88.4	1049	13	BM546790 AGENCOURT
8	88.4	88.4	1211	14	BM926296 AGENCOURT
9	87.4	87.4	455	14	W21335 zb55f03.r1
10	86.8	86.8	472	12	BE838990 RC6-FN013
11	65.4	65.4	552	9	AI255604 u156a05.y
12	65.4	65.4	536	13	B1328381
13	65.4	65.4	758	13	B1257017
14	65.4	65.4	771	12	BF384882
15	65.4	65.4	744	12	BF532104
16	65.4	65.4	875	12	BF385197
17	62.8	62.8	790	12	BF335332
18	53.6	53.6	638	13	B146007
19	39	39.0	538	12	BG641612
20	39	39.0	640	12	BG641885
21	39	39.0	640	13	B1468182
22	37.6	37.6	1061	17	CNS0339PM
23	36.4	36.4	638	10	AM133828
24	36.2	36.2	641	13	BM427276
25	35.6	35.6	900	13	BM438559
26	33	33.0	325	9	AA176034
27	33	33.0	433	10	BB796863
28	33	33.0	687	9	AV285869
29	32.2	32.2	834	17	CNS028M1
30	32	32.0	285	9	AI449301
31	31.6	31.6	304	9	AI852041
32	31.4	31.4	349	10	BB798742
33	31.4	31.4	359	10	BB804261
34	31.4	31.4	385	10	BB806529
35	31.4	31.4	956	12	BG122154
36	30.8	30.8	206	12	BF912734
37	30.8	30.8	295	9	AA293295
38	30.8	30.8	543	12	BG170842
39	30.8	30.8	602	14	BM951218
40	30.8	30.8	679	14	BQ330929
41	30.8	30.8	720	13	B1552439
42	30.8	30.8	724	13	B1547738
43	30.8	30.8	749	13	BM050541
44	30.8	30.8	776	13	B1833415
45	30.8	30.8	848	13	B1752594

ALIGNMENTS

RESULT 1
BE839155/c
LOCUS RC6-FN0138-110800-012-E07 FN0138 Homo sapiens CDNA, mRNA sequence.
ACCESSION BE839155
VERSION BE839155.1 GI:10271442
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=6t2-RC6-FN0138-110
 800-012-E07&t3=2000-08-11&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 18
 High quality sequence stop: 352.

FEATURES

Location/Qualifiers
 1..407

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="FN0138"
 /dev_stage="Adult"

/note="Organ: prostate,normal; Vector: puc18; Site_1: SmaI
 ; Site_2: SmaI; A mini-library was made by cloning
 products derived from ORESTES PCR (U.S. Letters Patent
 application No. 196,716 - Ludwig Institute for Cancer
 Research) profiles into the puc 18 vector. Reverse
 transcription of tissue mRNA and cDNA amplification were
 performed under low stringency conditions."

BASE COUNT

64 a 123 c 107 g 113 t

ORIGIN

Query Match 88.4%; Score 88.4; DB 12; Length 407;
 Best Local Similarity 98.9%; Pred. No. 4.9e-16;
 Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 11 AGTCACACGGAAGCTCTGCAGCTGACCAAGGAGAGCTGACAGCTCTGCCACAGGA 70
 Db 210 ATTACACAGGAAGCTCTGCAGCTGACCAAGGAGAGCTGACAGCTCTGCCACAGGA 151
 OY 71 ACAGAACTCTGTGTGTGTCTCTCTCCGCCCG 100
 Db 150 ACAGAACTCTGTGTGTGTCTCTCTCCGCCCG 121

RESULT 2

LOCUS

716 bp mRNA linear EST 25-SEP-2001
 B1757668

DEFINITION 603028107F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5198760 5',
 mRNA sequence.

ACCESSION B1757668
 VERSION B1757668.1 GI:15749246

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 716)
 NIH-MGC http://mgs.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov

Tissue procurement: Life Technologies, Inc.

CDNA library preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1497 row: m column: 01

High quality sequence stop: 716.

Location/Qualifiers
 1..716

FEATURES

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="5198760"
 /clone_lib="NIH_MGC_114"
 /lab_host="DH10B"

/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source anonymous pool of 6

male brains, age range 23-27 yo. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.5 kb. Insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 019. Note:
 this is a NIH-MGC Library."

BASE COUNT 189 a 204 c 210 g 113 t

ORIGIN

Query Match 88.4%; Score 88.4; DB 13; Length 716;
 Best Local Similarity 98.9%; Pred. No. 6.5e-16;
 Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 11 AGTCACACGGAAGCTCTGCAGCTGACCAAGGAGAGCTGACAGCTCTGCCACAGGA 70
 Db 369 ATTACACAGGAAGCTCTGCAGCTGACCAAGGAGAGCTGACAGCTCTGCCACAGGA 428
 OY 71 ACAGAACTCTGTGTGTGTCTCTCTCCGCCCG 100
 Db 429 ACAGAACTCTGTGTGTGTCTCTCTCCGCCCG 458

RESULT 3

LOCUS

844 bp mRNA linear EST 16-FEB-2001
 AL553470

DEFINITION AL553470 LIT_NFL006_PL2 Homo sapiens cDNA clone CSOD1076VA10 5
 prime, mRNA sequence.

ACCESSION AL553470
 VERSION AL553470.1 GI:12893334

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 844)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
 Unpublished (2001)

CONTACT: Genoscope
 Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr.

FEATURES

Location/Qualifiers
 1..844

SOURCE

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="CSOD1076VA10"
 /clone_lib="LIT_NFL006_PL2"
 /tissue_type="Placenta"

/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact: Feng Liang Life Technologies,
 Rockville, Maryland 20850, USA fax: (1) 301 610 8371

Email: fliang@lifestech.com URL: <http://fulllength.invitrogen.com>

BASE COUNT 221 a 231 c 244 g 137 t 11 others

ORIGIN

Query Match 88.4%; Score 88.4; DB 9; Length 844;
 Best Local Similarity 98.9%; Pred. No. 7e-16;
 Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 11 AGTCACACGGAAGCTCTGCAGCTGACCAAGGAGAGCTGACAGCTCTGCCACAGGA 70
 Db 398 ATTACACAGGAAGCTCTGCAGCTGACCAAGGAGAGCTGACAGCTCTGCCACAGGA 457
 OY 71 ACAGAACTCTGTGTGTGTCTCTCTCCGCCCG 100

1

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/clone_11b-LT1_NFL006_PL2"
/tissue_type="Placenta"
/note="Vector: pCMWSPORT 6: Site_1: NotI: 1st strand cDNA
was primed with a NotI-oligo(dt) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMWSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Peng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : filiang@lifetech.com url :
http://fulllength.invitrogen.com"

```

	Query Match	Best Local Similarity	Matches	Conservative	Score 88.4%	DB %	Length 984
Oy	11	ACTCACACGAGAGCTCTGCAGCCTGGACACAGGGGAGCTGACACATTTTCGCACACAGCA	70	1	1	1	1
2	432	ATTCAACAGGAGAGCTCTGCAGCCTGGACACAGGGAGCTGTGACCACTTTGCGACACAGGA	491	1	1	1	1
Oy	71	ACAGAGCTGTGTGTGTCTGCTCTGGGCGCG	100	1	1	1	1
Db	492	ACGAGACTGTGTGTGTCTCTCTGGGCGCG	521	1	1	1	1

RESULT	7
BMS46790	
LOCUS	BMS46790 1049 bp mRNA linear EST 20-FEB-2002
DEFINITION	AGNCOURT_6491143 NIH_MGC_125 Homo sapiens cDNA IMAGE:5733510
ACCESSION	5' , rRNA sequence.
VERSION	BMS46790 BMS46790
KEYWORDS	BMS46790.1 GI:18780039
SOURCE	EST.
ORGANISM	human.
	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1049)				
NIH-MGC http://mgc.ncbi.nlm.nih.gov/				
National Institutes of Health, Mammalian Gene Collection (MGC)				
Unpublished (1999)				
Contact: Robert Strausberg, Ph.D.				

Email: cgabs-remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
plate: LLAM12711 row: e column: 15
High quality sequence stop: 759.
Location/Qualifiers
I..1049

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5723510"
/clone_11d="NH_MGC_125"
/lab_host="DH10B"
/note="Organ: ovary (pool of 3); Vector: pCMV-Sport6;
Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1.3-5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."

```

	Query Match	Best Local Similarity	Score	DB	Length
Matches	89;	Conservative	88.4%; 98.9%;	Pred. No. 7.8e-16; Mismatches 1;	Indels 0; Gaps 0;
Qy	11	ACTCACACGGAACTTCGTGCAGCCTCGACACAACGCGGCACTGTGAACATTTGTGCACAGAGA	70		
Dd	426	ATTTCACAGGGAAGCTTGTGCAGCTTGACACACAGGGGCACTGTGACCACATTTGCCACAGAGA	485		
Qy	71	ACAGAACTCTGTGTGTGCTTCCTGCGCCG	100		
Dd	486	ACAGAACTCTGTGTGTGCTTCCTGCGCCG	515		

RESULT 8	BM926296	1211 bp	mRNA	linear	EST 12-MAR-2002
LOCUS	BM926296				
DEFINITION	AGGECOURT_6600735 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:57646598				
ACCESSION	5', mRNA sequence.				
VERSION	BM926296				
KEYWORDS	BM926296.1 GI:19376675				
SOURCE	EST.				
ORGANISM	human.				
	Homo sapiens				
	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 1211)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D.				

Email: cgapdb-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
 Clone distribution by: Agencourt Bioscience Corporation
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LLM12818 row: 1 column: 19
 High quality sequence: 529.
 location/Qualifiers

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SOURCE
1. 1211
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5764698"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
/note="Organ: brain; Vector: PCMV-SpOrt6; Site:1: Notif; Site:2: ECoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (ECoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Intelligen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."
BASE COUNT
296 a 351 c 351 g 211 t 2 others
ORIGIN

```

Query Match	88.4%	Score 88.4	DB 14	Length 1211
Best Local Similarity	98.9%	Pred. No. 8.3e-16		
Matches 89:	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY	11 AGTCACACGGAAGCTCTGTCAAGCTTGACACGGGAGCTGTGCCATCTCTGCACAGAGA	70		
Dd	392 ATTACACACGGAAAGCTTCTCAGCTTCGACACACGGGAGACTGTGCCAGTTCTGCACAGAGA	451		
QY	71 ACAGAACTCTGTGGTGTGCTCCTGGCCCG	100		
Dd	452 ACAGAACTCTGTGGTGTGCTCCTGGCCCG	481		

RESULT 9	W21335	455 bp	mRNA	linear	EST 20-AUG-1996
LOCUS	W21335				
DEFINITION	ZB55f03.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:307517 5' similar to gb:M57285 COAGULATION FACTOR X PRECURSOR (HUMAN);, mRNA sequence.				
ACCESSION	W21335				
VERSION	W21335.1				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 455) Hillier,L., Lemon,G., Becker,M., Bonaldo,M.F., Chiappelli,B., Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Philry,Meg.J., Treviski,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.				
TITLE	Generation and analysis of 280,000 hu in expressed sequence tags Genome Res. 6 (9), 807-828 (1996)				
JOURNAL	97044478				
MEDLINE	Contact: Wilson RK				
COMMENT	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1028 Std Error: 0.00 Seq primer: mob.REGA+ET High quality sequence stop: 424. Location/Qualifiers 1..455 /organism="Homo sapiens" /db_xref="GDB:1250929" /db_xref="taxon:9606" /clone="IMAGE:307517" /clone_11b="Soares_fetal_lung_NbHL19W" /dev_stage="19 weeks" /lab_host="DH10B (ampicillin resistant)" /note="Organ: lung; Vector: pTR73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer 15'-GTTCACCAATCTGACATGCGAGCGAGCCGCAATTTTCTTTTCTTTT-3', double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTR73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Patima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NBHL19W."				
BASE COUNT	116 a 135 c 131 g 69 t 4 others				
ORIGIN					
Query Match	87.4%: Score 87.4; DB 14; Length 455;				
Best Local Similarity	98.9%: Pred. No. 1e-15;				
Matches	88: Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	11 AGTCACACGGAAGCTCTGACAGCTTGAGACACGGGACATGTGACACAGTTCTGCACAGAGA 70				
Db	96 ATTTCACACGGAAGCTCTGACAGCTTGAGACACGGGACATGTGACACAGTTCTGCACAGAGA 155				
QY	71 ACAGAACTCTGTGTGCTCTCTGCGCC 99				
Db	156 ACAGAACTCTGTGTGCTCTCTGCGCC 184				

LOCUS	BE838990	472 bp	mRNA	linear	EST 22-SEP-2000
DEFINITION	RC6-FN0138-260700-011-G08 FN0138	Homo sapiens	CDNA	mRNA sequence.	
ACCESSION	BE838990				
VERSION	BE838990.1	GI:10271368			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 472)				
	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Grunstein, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brustein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J. G.				
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed				
JOURNAL	sequence tags				
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)				
COMMENT	20202663				
	Contact: Simpson A.J.G.				
	Laboratory of Cancer Genetics				
	Ludwig Institute for Cancer Research				
	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil				
	Tel: +55-11-2704922				
	Fax: +55-11-2707001				
	Email: asimpson@ludwig.org.br				
	This sequence was derived from the FAPESP/ICR Human Cancer Genome Project. This entry can be seen in the following URL				
	(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=612-RC6-FN0138-260700-011-G08&f3=2000-07-26&t4=1)				
	Seq primer: puc 18 forward				
	High quality sequence start: 9				
	High quality sequence stop: 307.				
FEATURES	Location/Qualifiers				
SOURCE	1..472				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/clone_lib="FN0138"				
	/dew_stage="Adult"				
	/note="Organ: prostate; normal; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."				
BASE COUNT	105 a 144 c 106 g 117 t				
ORIGIN					
Query Match	86.8%; Score 86.8; DB 12; Length 472;				
Best Local Similarity	97.8%; Pred. No. 1,6e-15;				
Matches	88; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
QY	11 AGTCACAGGAAGCTCTCAGCCTTGACAACAGGGAGACTGTGACCGATTCTGCCACAGAGA 70				
Db	192 ATTCTACAGGAGGAGCTCTCGCGCTTGACAACCGGAGACTGTGACCGATTCTGCCACAGAGA 133				
QY	71 ACAGAACTCTGTGTGTGCTCTCTCGGCGCCG 100				
Db	132 ACAGAACTCTGTGTGTGCTCTCTCTCGGCGCCG 103				
RESULT 11					
LOCUS	A1255604	552 bp	mRNA	linear	EST 12-NOV-1998
DEFINITION	u156a05.v1 Sugano mouse liver mla msa musculus CDNA clone				
ACCESSION	A1255604				
VERSION	A1255604.1	GI:3863129			
KEYWORDS	EST.				

SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
1 (bases 1 to 552)

AUTHORS Maira, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE The WashU-HMI Mouse EST project

JOURNAL Unpublished (1996)

COMMENT Contact: Maira M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu

FEATURES This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:970708
Seq primer: custom primer used
High quality sequence stop: 511.

FEATURES
source
1..552
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1886384"
/clone_1ib="Sugano mouse liver mlia"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: liver; Vector: pME18S-FL3; Site:1: DraIII (CACTGTGTG); Site:2: DraIII (CACCAGTGTG); 1st strand cDNA was primed with an oligo(dT) primer
[ATGCGCCCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCTCTAGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCAGTGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTTCTCTATAAGCTGCG and 3' end primer CGACTGCGAGCTCGGACACA."

BASE COUNT 147 a 129 c 156 g 120 t

ORIGIN

Query Match 65.4%; Score 65.4; DB 9; Length 552;
Best Local Similarity 86.7%; Pred. No. 3.7e-09;
Matches 72; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 18 CGGAAGCTCTGAGCTGAGCAACGGGAGCTGTGACCACTTCTGCCAGCAGACGAGAAC 77
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 390 CGGAAGCTCTGAGCTGAGCAACGGGAGCTGTGACCACTTCTGCCAGCAGACGAGAAC 449
QY 78 TCTGTGTGTGTCTCTCTGCGCCGC 100
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 450 TCAGTGTGTGTCTCTCTGCGCCGCAG 472

RESULT 12
LOCUS B1328381 596 bp mRNA linear EST 30-JUL-2001
DEFINITION 60298581F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:5138306 5',
mRNA sequence.
ACCESSION B1328381
VERSION B1328381.1 GI:15013038
KEYWORDS EST
SOURCE house mouse.
ORGANISM Mus musculus

SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
1 (bases 1 to 596)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL1340 row: f column: 03
High quality sequence stop: 594.

FEATURES
source
1..596
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5138306"
/clone_1ib="NCI_CGAP_L19"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-Sport6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 159 a 140 c 169 g 128 t

ORIGIN

Query Match 65.4%; Score 65.4; DB 13; Length 596;
Best Local Similarity 86.7%; Pred. No. 3.8e-09;
Matches 72; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 18 CGGAAGCTCTGAGCTGAGCAACGGGAGCTGTGACCACTTCTGCCAGCAGACGAGAAC 77
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 384 CGGAAGCTCTGAGCTGAGCAACGGGAGCTGTGACCACTTCTGCCAGCAGACGAGAAC 443
QY 78 TCTGTGTGTGTCTCTCTGCGCCGC 100
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 444 TCAGTGTGTGTCTCTCTGCGCCGCAG 466

RESULT 13
LOCUS B1257017 758 bp mRNA linear EST 20-JUL-2001
DEFINITION 602978857F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:5123607 5',
mRNA sequence.
ACCESSION B1257017
VERSION B1257017.1 GI:14811984
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
1 (bases 1 to 758)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)

AUTHORS Unpublished (1999)

TITLE Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL1302 row: a column: 16
High quality sequence start: 3
High quality sequence stop: 756.

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OM nucleic - nucleic search, using sw model

Run on: January 15, 2003, 17:50:20 ; Search time 151 Seconds
(without alignments)
1491.390 Million cell updates/sec

Title: 100394_COPY_1_100

Perfect score: 100
Sequence: 1 CTCCTTGGCAGTCACACGG.....GTGTGTGCTCTGCGCCG 100

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq.101002.*

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11:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
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18:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
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21:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT.*
23:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24:	/SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	100.0	367	21	AAC70860
2	99.6	99.6	367	21	AAC70878
3	99.6	99.6	367	21	AAC70884
4	88.4	88.4	788	12	AAQ12776
5	88.4	88.4	1126	20	AAK15427
6	88.4	88.4	1126	21	AAH89786
7	88.4	88.4	1126	21	AAH12970
8	88.4	88.4	1126	21	AAZ56120
9	88.4	88.4	1404	19	AAV10462

10	88.4	88.4	1467	19	AAV56776	Human Factor X gen
11	88.4	88.4	1467	19	AAV56821	Human Factor X gen
12	88.4	88.4	1467	19	AAV59409	Human factor X nuc
13	88.4	88.4	1507	21	AAA54031	Human factor X cod
14	88.4	88.4	1887	21	AAH57469	Human liver cell s
15	85.4	85.4	300	22	AAH57261	Human liver specif
16	82.8	82.8	1560	22	AAE24735	Nucleotide sequenc
17	82.8	82.8	1660	22	AAE24738	Nucleotide sequenc
18	52.4	52.4	1554	15	AAO71243	Serine protease fo
19	31.8	31.8	13923	23	ABL05109	Drosophila melanog
20	31.8	31.8	17902	23	ABL05108	Drosophila melanog
21	30.8	30.8	295	24	ABL80210	Human ovarian can
22	30.8	30.8	2461	17	AAE41544	Human gase-encodin
23	29.6	29.6	4790	22	AAE41544	Human gase-encodin
24	29.6	29.6	4790	22	AAE41544	Human gase-encodin
25	29.4	29.4	4181	22	AAO06778	Human haematopoiet
26	29.4	29.4	4801	22	AAO06778	Human haematopoiet
27	29.2	29.2	1743	23	AAH85732	DNA encoding novel
28	29.2	29.2	2196	23	AAH85732	DNA encoding novel
29	29.2	29.2	2196	23	AAH85733	DNA encoding novel
30	29.2	29.2	2196	23	AAH85733	DNA encoding novel
31	29.2	29.2	2196	23	AAH85733	DNA encoding novel
32	29.2	29.2	2196	23	AAH85733	DNA encoding novel
33	29.2	29.2	2196	23	AAH85733	DNA encoding novel
34	29.2	29.2	2196	23	AAH85733	DNA encoding novel
35	29.2	29.2	2196	23	AAH85733	DNA encoding novel
36	29.2	29.2	2196	23	AAH85733	DNA encoding novel
37	29.2	29.2	2196	23	AAH85733	DNA encoding novel
38	29.2	29.2	2196	23	AAH85733	DNA encoding novel
39	29.2	29.2	2196	23	AAH85733	DNA encoding novel
40	29.2	29.2	2196	23	AAH85733	DNA encoding novel
41	29.2	29.2	2196	23	AAH85733	DNA encoding novel
42	29.2	29.2	2196	23	AAH85733	DNA encoding novel
43	29.2	29.2	2196	23	AAH85733	DNA encoding novel
44	29.2	29.2	2196	23	AAH85733	DNA encoding novel
45	29.2	29.2	2196	23	AAH85733	DNA encoding novel

ALIGNMENTS

RESULT 1	
1	AAC70860
ID	AAC70860 standard; DNA; 367 BP.
XX	
AC	AAC70860;
XX	
DT	09-FEB-2001 (first entry)
DE	Single nucleotide polymorphism containing sequence #230.
XX	
KW	Single nucleotide polymorphism; SNP; human; genetic disease;
KW	disease susceptibility; cardiovascular system; endocrine system;
KW	neurological system; forensic testing; paternity testing; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200058519-A2.
XX	
PD	05-OCT-2000.
XX	
PF	30-MAR-2000; 2000MO-US08440.
XX	
PR	31-MAR-1999; 99US-0127248.
XX	
PA	(WHED) WHITEHEAD INST BIOMEDICAL RES.
PA	(AFY-) AFFYMETRIX INC.
XX	
PI	Altshuler D, Cargill M, Daley GO, Ireland JS, Lander ES;
XX	Lipshutz RJ, Patil N, Sklar P;
DR	WPI; 2000-611722/58.

Claim 1; Fig 5; 21app; English.

Claim 1; Fig 5; 21app; English.

The present invention is concerned with a number of human single nucleotide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosis and prediction of an individual's susceptibility to disease, in forensic and paternity testing and in genetic mapping. In particular, the SNPs of the invention can be

ID	AAV56821 standard; DNA; 1467 BP.
XX	AAV56821;
AC	AAV56821;
XX	27-NOV-1998 (first entry)
DT	27-NOV-1998 (first entry)
XX	Human Factor X genomic DNA.
DE	Human Factor X genomic DNA.
XX	Factor X; analogue; activation cleavage site; protease; bleeding; human;
KM	Factor IX; Factor VII; Factor VIII; haemophilia; gene therapy; ss.
XX	Factor IX; Factor VII; Factor VIII; haemophilia; gene therapy; ss.
OS	Homo sapiens.
XX	Homo sapiens.
FH	Key
FT	CDS
FT	Location/Qualifiers
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FT	/*tag= a
FT	sig_peptide
FT	1..120
FT	/*tag= b
FT	mat_peptide
FT	121..1464
FT	/*tag= C
FT	/product= "Factor X"
..X	
PN	MO9838318-A1.
XX	03-SEP-1998.
PD	03-SEP-1998.
XX	27-FEB-1998;
FF	98WO-AT00046.
XX	27-FEB-1998;
PR	97AT-0000336.
XX	27-FEB-1997;
PA	(IMMO) IMMUNO AG.
XX	
PI	Dorner F, Elbl J, Falkner F, Himmelsbach M, Pfeiderer M;
PI	Schlokat U;
DR	WP1: 1998-481212/41.
DR	P-PSDB: AAW76218.
XX	
XX	New factor 10 deletion mutants lacking the natural protease
PT	processing site - but having a non-natural site inserted, and
PT	related DNA, particularly for in vitro activation to products used
PT	to treat blood coagulation disorders
XX	
PS	Claim 3; fig 1; 82pp; German.
XX	
CC	This sequence encodes the human Factor X protein which is used in a
CC	method resulting in the production of novel human Factor X (F10)
CC	analogues. Such analogues have in the region of the natural F10a
CC	activation cleavage site, a modification that creates a processing site
CC	for a protease that does not naturally cleave F10 in this region. The
CC	proteins are used to generate, in vivo or in vitro, F10a analogues that
CC	can be used to control bleeding and for treating defects of factors IX,
CC	VIII or VIII, e.g. in haemophiliacs who have developed antibodies to
CC	factors VIII and/or IX. The encoding nucleic acid can be used in gene
CC	therapy of the same conditions. The analogues have high stability and can
CC	be activated without use of animal enzymes such as trypsin. Only
CC	activation is affected, their activity is the same as the natural factor.
CC	The analogues can be isolated as a pure single-chain pro-protein (not
CC	usually possible because of rapid processing of the native precursor) and
CC	this converted to two-chain form by subsequent activation. Activated
CC	analogues have good stability and structural integrity and are
CC	practically free of inactive intermediates and autolytic
CC	decomposition products.
XX	
SO	Sequence 1467 BP; 363 A; 424 C; 444 G; 236 T; 0 other;
QY	Query Match 88.4%; Score 88.4; DB 19; Length 1467;
	Best Local Similarity 98.9%; Pred. No. 2e-18;
Matches	89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
11	AGTACACGGAAGCTCTGACGCTGGACAACGGGGACGTGTGACCACTTCTGCACAGAGA 70
369	ATTTCACACGGAAGCTCTGACGCTGGACAACGGGGACGTGTGACCACTTCTGCACAGAGA 428

```

OY      71 ACAGAACTGTGTGTCTCTCTGCGCCG 100
        |||||||
DB      429 ACAGAACTGTGTGTCTCTCTGCGCCG 458

RESULT 12
ID      AAF59409 standard; cDNA: 1467 BP.
AC      AAF59409;
NC      AAF59409;
DT      02-MAY-2001 (first entry)
DE      Human factor X nucleotide sequence SEQ ID NO:1.
KW      Human; factor X; mutant; haemostatic; gene therapy; haemophilia;
KW      blood coagulation disorder; haemophilia; ss.
OS      Homo sapiens.
PN      WO200110896-A2.
PD      15-FEB-2001.
PR      07-AUG-2000; 2000WO-EP07631.
PR      10-AUG-1999; 99AT-0001377.
PA      (BAXT ) BAXTER AG.
PI      Himmelspach M, Schlokot U;
        MPI: 2001-191516/19.
DR      P-PSDB; AAB70411.
PT      Novel factor X analog useful for producing drug which is useful for
PT      treatment of blood coagulation disorders, such as hemophilia, contains
PT      modification between amino acids Glu226 and Ile235 -
XX      Disclosure: Fig 1; 50pp; English.
XX
XX      The present invention describes a factor X analogue (I) which contains
XX      a modification between Glu226 and Ile235, relative to the 488 residue
XX      amino acid sequence given in AAB70411. (I) has haemostatic activity and
XX      can be used in gene therapy. (I) encoding polynucleotide (II) can be
XX      used to produce a drug, which is useful for treatment of patients with
XX      blood coagulation disorders, such as patients suffering from haemophilia,
XX      or haemophilias with inhibitory antibodies. Preparations containing a
XX      polypeptide with factor X/Xa activity are more readily activated by
XX      factor Xla or its derivative, which has high stability, without having
XX      to use one of the proteases used in prior art to activate the natural
XX      factor X, particularly one of animal origins, such as Russell's viper
XX      venom (RVV) or trypsin. The present sequence encodes human factor X,
XX      which is given in the exemplification of the present invention.
XX
XX      Sequence 1467 BP: 363 A: 424 C: 444 G: 236 T: 0 other:
XX
XX      Query Match      88.4%; Score 88.4; DB 22; Length 1467;
XX      Best Local Similarity 98.9%; Pred. No. 2e-18;
XX      Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0.0;
OY      11 AGTCACAGGAAAGCTCTGAGCGTGGACACGGGGGAGCTGTGACCACTGTGCACAGAGA 70
        |
DB      369 ATTTCACAGGAAAGCTCTGAGCGTGGACACGGGGGAGCTGTGACCACTGTGCACAGAGA 428
OY      71 ACAGAACTGTGTGTCTCTCTGCGCCG 100
        |||||||
DB      429 ACAGAACTGTGTGTCTCTCTGCGCCG 458

RESULT 13
AAAS4031

```


RESULT 15

AAH57261 standard; cDNA: 300 BP.

AAH57261;

10-SEP-2001 (first entry)

Human liver specific cDNA sequence SEQ ID NO:101.

Human: tissue specific; diagnosis; brain; heart; skeletal muscle; lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss; metabolic disease; developmental disease; cytostatic; immunomodulatory; neuroprotective; gene therapy; cancer; immunopathology; neuropathology.

Homo sapiens.

W0200132927-A2.

10-MAY-2001.

02-NOV-2000; 2000WO-US30396.

04-NOV-1999; 99US-0163508.

(INCYTE) INCYTE GENOMICS INC.

Sornasse T, Sellhamer JJ, Watson GA;

WPI; 2001-291057/30.

New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene is associated with a cancer, immunopathology or neuropathology -

Claim 1; Page 107; 327pp; English.

AAH57161 to AAH57576 represent cell and tissue specific polynucleotide sequences (I). (I) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (I) and proteins (II) encoded by then are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids, mimetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of (I) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene is associated with a cancer, immunopathology or neuropathology.

Sequence 300 BP; 73 A; 81 C; 88 G; 44 T; 14 other;

Query Match

85.4%; Score 85.4; DB 22; Length 300;

Best Local Similarity 95.6%; Pred. No. 1,2e-17;

Matches 86; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 11 AGTCACACGGAAGCTGTGACCTGTGACACGAGGAGCTGTGACAGTTCCTCCACGAGAGA 70

Db 16 ATTANANAGGAAGCTGTGAGCTGTGACACGAGGAGCTGTGACAGTTCCTCCACGAGAGA 75

QY 71 ACAGAACTCTGTGTGGTGGCTGTGCGCCGCCG 100

Db 76 ACAGAACTCTGTGTGGTGGCTGTGCGCCGCCG 105

Search completed: January 15, 2003, 19:50:15
Job time : 154 secs

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

(without alignments)
2181.620 Million cell updates/sec

Title: L00394_COPY_1_100

Sequence: 1 CTCCTTTGGCAGTCACACGG.....GTGGTGTGCTCCTGCGCCCG 100

Scoring table:	IDENTITY_NUC	Gapcost 1 0
	Gapcost 10 0	

Searched: 2054640 seqs, 14551402878 residues

total number of hits satisfying chosen parameters: 4109280

Minimum	DB	seq	length:	0
Maximum	DB	seq	length:	3

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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3:	gb_hlg:*
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8:	gb_pl1:*
9:	gb_pr:*
10:	gb_pro:
11:	gb_srs:*
12:	gb_sy:*
13:	gb_un:*
14:	gb_v1:*
15:	emb_da:
16:	emb_fm:
17:	emb_hum:
18:	emb_in:*
19:	emb_on:
20:	emb_un:
21:	emb_or:*
22:	emb_ov:*
23:	emb_pat:*
24:	emb_ph:
25:	emb_pl1:*
26:	emb_pro:
27:	emb_srs:
28:	emb_un:
29:	emb_v1:
30:	emb_hlg_hum:
31:	emb_hlg_inv:
32:	emb_hlg_other:
33:	emb_hlg_nus:
34:	emb_hlg_pln:
35:	emb_hlg_pro:
36:	emb_hlg_nam:
37:	emb_hlg_vrt:
38:	emb_sy:
39:	emb_hngo_hum:
40:	emb_hngo_nus:
41:	emb_hngo_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	100.0	156	HUMFX5	I00354 Human facti
2	93.8	93.8	29488	AF503510	AF503510 Homo sapi
3	93.8	93.8	132933	AL137002	AL137002 Human DNA
4	92	92.0	350	AB005892	AB005892 Homo sapi
5	88.4	88.4	1126	AR095306	AR095306 Sequence
6	88.4	88.4	1126	AR103990	AR103990 Sequence
7	88.4	88.4	1126	HUMFX	K10866 Human facti
8	88.4	88.4	1404	AG3124	AG3124 Sequence 15
9	88.4	88.4	1414	HUMGCX	M22613 Human blood
10	88.4	88.4	1443	HUMEXM	K03194 Human facti
11	88.4	88.4	1467	AB6859	AB6859 Sequence 43
12	88.4	88.4	1467	AB6866	AB6866 Sequence 26
13	88.4	88.4	1467	AX082959	AX082959 Sequence
14	88.4	88.4	1500	AR024194	AR024194 Sequence
15	88.4	88.4	1507	HUMFXCX	M57285 Human coagu
16	72.2	72.2	49581	AC131472	AC131472 Rattus no
17	69.4	69.4	20130	AF211347	AF211347 Mus muscu
18	69.4	69.4	299880	AC127308	AC127308 Mus muscu
19	68.6	68.6	1500	AF003200	AF003200 Oryctolag
20	66.6	66.6	1497	RNFXRAT	Y79607 R. norvegicu
21	65.4	65.4	1486	AF087644	AF087644 Mus muscu
22	65.4	65.4	1491	MGCCAGTUX	AF232677 Mus muscu
23	65.4	65.4	1925	BC003877	BC003877 Mus muscu
24	52.4	52.4	1537	BTCFX1	X06673 Bovine mRNA
25	52.4	52.4	1554	A73583	A73583 Sequence 1
26	52.4	52.4	1554	AR001423	AR001423 Sequence
27	45.4	45.4	1599	AF275654	AF275654 Oritolbor
28	40.2	40.2	20947	AF519546	AF519546 Dantio rer
29	33.4	32.4	2246	CHKVPB	DD0844 Gallus gall
30	31.8	31.8	133171	AC008370	AC008370 Drosophil
31	31.8	31.8	134370	AC108106	AC108106 Homo sapi
32	31.8	31.8	157559	AC020344	AC020344 Drosophil
33	31.8	31.8	226833	AE003838	AE003838 Drosophil
34	30.8	30.8	1558	OCU49933	OCU49933 Oryctolag
35	30.8	30.8	2461	123785	Sequence 1
36	30.8	30.8	2461	HUMGAS	I13720 Homo sapien
37	30.6	30.6	126721	AC118793	AC118793 Rattus no
38	30.6	30.6	159743	AC126937	AC126937 Mus muscu
39	30.2	30.2	148198	AC024432	AC024432 Homo sapi
40	30.2	30.2	218138	AC122193	AC122193 Mus muscu
41	30	30.0	96642	AC002291	AC002291 Arabidops
42	30	30.0	203200	AC008744	AC008744 Homo sapi
43	29.6	29.6	6846	AB011540	AB011540 Homo sapi
44	29.6	29.6	113228	AL513015	AL513015 Human DNA
45	29.6	29.6	114191	AL451007	AL451007 Human DNA

ALIGNMENTS

RESULT 1	
HUMFX5	
LOCUS	156 bp DNA linear PRI 09-NOV-1994
DEFINITION	Human factor X (blood coagulation factor) gene, exon 5.
ACCESSION	L00394 M14327
VERSION	L00394.1 GI:182826
KEYWORDS	Stuart factor; blood coagulation factor; factor X; glycoprotein; serine protease.
SEGMENT	5 of 8
SOURCE	Homo sapiens (tissue library: of Lawn et al., and Yoshitake et al.) cDNA.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. (bases 1 to 156)

```

AUTHORS      Leytus,S.P., Foster,D.C., Kurachi,K. and Davie,E.W.
TITLE         Gene for human factor X: a blood coagulation factor whose gene
              organization is essentially identical with that of factor IX and
              protein C
JOURNAL       Biochemistry 25 (18), 5098-5102 (1986)
MEDLINE       87026600
PUBMED        3768336
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              BASE COUNT      32 a      49 c      48 g      27 t
              ORIGIN      About 1.8 kb after segment 4; chromosome 13q34.
              Query Match      100.0%; Score 100; DB 9; Length 156;
              Best Local Similarity 100.0%; Pred. NO. 1.5e-19;
              Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CTCCTTTGGAGTACACGGAAGCTCTGCAGCTGACACAAAGGGGACTGTACACAGTCTCT
Db      1 CTCCTTTGGAGTACACGGAAGCTCTGCAGCTGACACAAAGGGGACTGTACACAGTCTCT
QY      61 GCCACGAGAACAGAACTGTGTGTGTCTCTCTGCGCCG 100
Db      61 GCCACGAGAACAGAACTGTGTGTGTCTCTCTGCGCCG 100
RESULT 2
AF503510      29488 bp      DNA      linear      PRI 22-MAY-2002
LOCUS      AF503510
DEFINITION      Homo sapiens coagulation factor X (F10) gene, complete cds.
ACCESSION      AF503510
VERSION      AF503510.1 GI:20336662
KEYWORDS
SOURCE      Homo sapiens.
              Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 29488)
              Rieder,M.J., Armel,T.Z., Carrington,D.P., Chung,M.-W., Lee,K.L.,
              Ozuna,M., Poel,C.L., Toth,E.J., Yi,Q. and Nickerson,D.A.
              Direct Submission
              Submitted (17-APR-2002) Genome Sciences, University of Washington,
              1705 NE Pacific, Seattle, WA 98195, USA
              To cite this work please use: SeattleSNPs, NHLBI HL66682 Program
              for Genomic Applications, UW-FHCRC, Seattle, WA (URL:
              http://pga.gs.washington.edu).
FEATURES      Location/Qualifiers
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                /replace="a"
              variation
                577

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was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr13>
RP11-98F14 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pBAC3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-98F14. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true left end of clone RP11-98F14 is at 1 in this sequence. The true left end of clone RP11-391H12 is at 122834 in this sequence. The true right end of clone RP11-265C7 is at 123923 in this sequence.

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FEATURES
source          1..132933
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                /clone_1fb="RPCI-11.1"
                /clone_1fb="RPCI-11.1"
                /note="Alu repeat: matches 1..229 of consensus"
                /note="3 copies 32 mer 93% conserved"
                /note="AluSg repeat: matches 1..307 of consensus"
                /note="1207
                1483..1912
                /note="CpG island"
                /evidence="not_experimental"
                /note="MER58A repeat: matches 19..167 of consensus"
                /note="2703..2861
                /note="L1M3e repeat: matches -118..34 of consensus"
                /note="4371..4978
                /note="38 copies 16 mer 78% conserved"
                /note="4374..4981
                /note="19 copies 32 mer 87% conserved"
                /note="6373..6448
                /note="2 copies 38 mer 93% conserved"
                /note="6411..6563
                /note="3 copies 51 mer 93% conserved"
                /note="6565..6669
                /note="3 copies 35 mer 85% conserved"
                /note="6612..6687
                /note="2 copies 38 mer 98% conserved"
                /note="6672..6773
                /note="2 copies 51 mer 93% conserved"
                /note="6852..6923
                /note="4 copies 18 mer 81% conserved"
                /note="8854..8988
                /note="15 copies 9 mer cccgaacc 63% conserved"
                /note="8860..8943
                /note="3 copies 28 mer 83% conserved"
                /note="8920..9059
                /note="4 copies 35 mer 75% conserved"
                /note="8927..9056
                /note="5 copies 26 mer 69% conserved"
                /note="8935..9002
                /note="4 copies 17 mer 95% conserved"
                /note="8984..9037
                /note="3 copies 18 mer 90% conserved"
                /note="9427..9530
                /note="4 copies 26 mer 92% conserved"
                /note="10204..10602
                /note="7 copies 57 mer 87% conserved"
                /note="11050..11091
                /note="2 copies 21 mer 100% conserved"
                /note="11469..11823
                /note="L1MCI repeat: matches 5862..6231 of consensus"
                /note="13157..13200
                /note="L1R5 repeat: matches 690..733 of consensus"
                /note="13006..14155
                /note="5 copies 70 mer 82% conserved"
                /note="15491..15973
                /note="CpG island"
                /evidence="not_experimental"
                /note="16278..16371
                /note="2 copies 47 mer 87% conserved"
                /note="16956..17159
                /note="4 copies 51 mer 95% conserved"
                /note="19411..19587
                /note="3 copies 59 mer 79% conserved"
                /note="20202..20342
                /note="3 copies 47 mer 96% conserved"
                /note="20473..20564
                /note="L2 repeat: matches 2602..2693 of consensus"
                /note="20816..21894
                /note="CpG island"
                /evidence="not_experimental"
                /note="24570..24680
                /note="L1M4 repeat: matches 3584..3686 of consensus"
                /note="24681..24999
                /note="Alu repeat: matches 1..311 of consensus"
                /note="25000..25306
                /note="L1M4 repeat: matches 3686..4029 of consensus"
                /note="25311..25620
                /note="Alu repeat: matches 1..311 of consensus"
                /note="25345..25989
                /note="CpG island"
                /evidence="not_experimental"
                /note="25755..26053
                /note="AluSg repeat: matches 1..304 of consensus"
                /note="27585..27688
                /note="4 copies 26 mer 74% conserved"
                /note="27733..27981
                /note="Alu repeat: matches 9..282 of consensus"
                /note="29431..29498
                /note="MER81 repeat: matches 4..72 of consensus"
                /note="29553..29870
                /note="AluSg repeat: matches 1..309 of consensus"
                /note="30907..31396
                /note="7 copies 70 mer 64% conserved"
                /note="30908..31432
                /note="15 copies 35 mer 61% conserved"
                /note="30911..31412
                /note="251 copies 2 mer 99 61% conserved"
                /note="30938..31413
                /note="17 copies 28 mer 61% conserved"
                /note="30973..31420
                /note="14 copies 32 mer 61% conserved"
                /note="30987..31385
                /note="7 copies 57 mer 64% conserved"
                /note="31000..31080
                /note="Sequence from uni-directional dGTP big dye
                terminator reads only."
                /note="31043..31413
                /note="7 copies 53 mer 63% conserved"
                /note="31078..31415
                /note="13 copies 26 mer 62% conserved"
                /note="31136..31417
                /note="6 copies 47 mer 66% conserved"
                /note="31152..31421
                /note="9 copies 30 mer 61% conserved"
                /note="31153..31267
                /note="Single clone region. Sequence from reads from a
                short insert library derived from a single pUC clone.
                Restriction digest data confirm the assembly."
                /note="31175..31426
                /note="12 copies 21 mer 61% conserved"
                /note="31268..31411
                /note="9 copies 16 mer 64% conserved"
                /note="31268
                /note="random repeat. Forced join. Gap size estimated to
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LOCUS	DEFINITION	VERSION	KEYWORDS	LOCUS	DEFINITION	VERSION	KEYWORDS
CDs	<77. .>208 /gene="F10" /codon_start=-1 /product="coagulation factor X" /protein_id="BAA21634.1" /db_xref="GI:2281791" /translation="SHGSAAMVTGTVTSSATRNRTLMCAPAPACTPMLTTARAPPC"			exon	77. .208 /gene="F10" /number=5 209. .350 /note="Intron E"		
intron				BASE COUNT	69 a 113 c 115 g 53 t		
ORIGIN				Query Match	92.0%: Score 92; DB 9; Length 350; Best Local Similarity 100.0%: Pred. No. 3.5e-17; Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	9 GCAGTCACACGGAAGCTCTGCAGCCTTGACAAACGGGGAGCTGTGACCACTTCTGCCACGAG 68			Db	73 GCAGTCACACGGAAGCTCTGCAGCCTTGACAAACGGGGAGCTGTGACCACTTCTGCCACGAG 132		
OY	69 GAACAGAACTCTGTGTGCTCTCTGCGCCCG 100			Db	133 GAACAGAACTCTGTGTGCTCTCTGCGCCCG 164		
RESULT 5				LOCUS	AR095306	1126 bp	DNA
LOCUS	AR095306	1126 bp	DNA	DEFINITION	sequence 27 from patent US 6004555.	linear	PAT 08-SEP-2000
ACCESSION	AR095306	GI:10023064		VERSION	AR095306.1	GI:10023064	
KEYWORDS	Unknown.			SOURCE	Unknown.		
ORGANISM	Unknown.			REFERENCE	1 (bases 1 to 1126) Thorpe,P.E. and Edgington,T.S. Methods for the specific coagulation of vasculature Patent: US 6004555-A 27 21-DEC-1999; Location/Qualifiers 1. .1126 /organism="unknown"		
BASE COUNT	269 a 341 c 342 g 174 t			ORIGIN			
Query Match	88.4%: Score 88.4; DB 6; Length 1126; Best Local Similarity 98.9%: Pred. No. 3.9e-16; Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			OY	11 AGTCACACGGAAGCTCTGCAGCCTTGACAAACGGGGAGCTGTGACCACTTCTGCCACGAGA 70		
Db	27 ATTTCACAGGAAGCTCTGCAGCCTTGACAAACGGGGAGCTGTGACCACTTCTGCCACGAGA 86			OY	71 ACAGAACTCTGTGTGCTCTCTGCGCCCG 100		
Db	87 ACAGAACTCTGTGTGCTCTCTGCGCCCG 116			RESULT 6			
LOCUS	ARI03990	1126 bp	DNA	LOCUS	ARI03990	1126 bp	DNA
DEFINITION	Sequence 27 from patent US 6093399.	linear	PAT 14-FEB-2001	DEFINITION	Sequence 27 from patent US 6093399.	linear	PAT 14-FEB-2001
ACCESSION	ARI03990			ACCESSION	ARI03990		
VERSION	ARI03990.1	GI:12816698		VERSION	ARI03990.1	GI:12816698	
KEYWORDS	Unknown.			KEYWORDS	Unknown.		
SOURCE	Unknown.			SOURCE	Unknown.		
ORGANISM	Unclassified.			ORGANISM	Unclassified.		

REFERENCE 1 (bases 1 to 1126)
 AUTHORS Thorpe,P.E. and Edgington,T.S.
 TITLE Methods and compositions for the specific coagulation of vasculature
 JOURNAL Patent: US 6093399-A 27 25-JUL-2000;
 FEATURES Location/Qualifiers
 source 1..1126 /organism="unknown"
 BASE COUNT 269 a 341 c 342 g 174 t
 ORIGIN
 Query Match 88.4%; Score 88.4; DB 6; Length 1126;
 Best Local Similarity 98.9%; Pred. No. 3.9e-16;
 Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 AGTCACAGGAGAGCTCTGACCTGACACGCGAGCTGTGACCAAGTTCTGCCACGAGA 70
 |
 DB 27 ATTACACAGGAGAGCTCTGACCTGACACGCGAGCTGTGACCAAGTTCTGCCACGAGA 86
 |
 QY 71 ACAGAACTCTGTGTGTCTCTCTGCGCCG 100
 |
 DB 87 ACAGAACTCTGTGTGTCTCTCTGCGCCG 116
 |

RESULT 7
 LOCUS HUMFX 1126 bp mRNA linear PRI 08-NOV-1994
 DEFINITION Human factor X mRNA.
 ACCESSION K01886
 VERSION K01886.1 GI:182820
 KEYWORDS Stuart factor; factor X; serine protease.
 SOURCE Human liver, cDNA to mRNA, clone lambda-X-1137.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1126)
 AUTHORS Leytus,S.P., Chung,D.W., Kiesel,W., Kurachi,K. and Davie,E.W.
 TITLE Characterization of a cDNA coding for human factor X
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 81 (12), 3699-3702 (1984)
 MEDLINE 84222026
 PUBMED 6587384

FEATURES
 source In processing, factor X (Stuart factor) is converted to Xa by cleavage of a glycopeptide from the amino-terminal end of the heavy chain. It then acts as a serine protease in converting prothrombin to thrombin.
 location/Qualifiers
 1..1126
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /map="13q34"
 1..1126
 /gene="F10"
 <1..1126
 /gene="F10"
 /product="factor X mRNA"
 <1..1116
 /gene="F10"
 /note="factor X precursor peptide"
 /codon_start=1
 /protein_id="AA552486.1"
 /db_xref="GI:182821"
 /db_xref="GDB:600-119-890"
 /translation="GPEGNCELFTRKLCSLDNGDODFCHEONSYSVCARGYTLDNGKACIPGPPYPCGKQTLRRKRSVAQNTSSSGEAPDSITWKPDAADLDPTENPDLDFNTOPEBDNNLTRIVGGECKDEGCPWALLINEENGPCGGTILSEFYLLTAACLVOAKREFGDRNTEOREGEAVEHVEVYVYKHNRTETETDPTIANVRLKPTPTFRMVAAPCLPERDMESTLNTQKTGIVSGGRTHERGROSTRLKMLEVPYVDNSCKLSSTFIIONMFCAGTIDKQDCAQGSQGPHTRFQDTYFVTGIVSWGECARKKYGIYKVTAFKMWIDRSMKTRGLPRAKSHAPVITSPK"
 <1..195
 /gene="F10"
 /product="factor X light chain"
 205..1113
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 mat_peptide

/gene="F10"
 /product="factor X heavy chain"
 361..1113
 mat_peptide
 /gene="F10"
 /product="factor Xa heavy chain"
 269 a 341 c 342 g 174 t
 ORIGIN 5 bp upstream of TaqI site.
 Query Match 88.4%; Score 88.4; DB 9; Length 1126;
 Best Local Similarity 98.9%; Pred. No. 3.9e-16;
 Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 AGTCACAGGAGAGCTCTGACCTGACACGCGAGCTGTGACCAAGTTCTGCCACGAGA 70
 |
 DB 27 ATTACACAGGAGAGCTCTGACCTGACACGCGAGCTGTGACCAAGTTCTGCCACGAGA 86
 |
 QY 71 ACAGAACTCTGTGTGTCTCTCTGCGCCG 100
 |
 DB 87 ACAGAACTCTGTGTGTCTCTCTGCGCCG 116
 |

RESULT 8
 LOCUS A93124 1404 bp DNA linear PAT 22-JAN-2000
 DEFINITION Sequence 15 from Patent WO9747737.
 ACCESSION A93124
 VERSION A93124.1 GI:6741514
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 1404)
 AUTHORS Kopeitzki,E. and Hopfner,K.
 TITLE RECOMBINANT BLOOD-COAGULATION PROTEASES
 JOURNAL Patent: WO 9747737-A 15 18-DEC-1997;
 KOPETZKI ERHARD (DE); BOEHRIINGER MANNHEIM GMBH (DE)
 FEATURES Location/Qualifiers
 source 1..1404
 /organism="unidentified"
 /db_xref="taxon:32644"

BASE COUNT 356 a 402 c 425 g 221 t
 ORIGIN
 Query Match 88.4%; Score 88.4; DB 6; Length 1404;
 Best Local Similarity 98.9%; Pred. No. 3.8e-16;
 Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 11 AGTCACAGGAGAGCTCTGACCTGACACGCGAGCTGTGACCAAGTTCTGCCACGAGA 70
 |
 DB 315 ATTACACAGGAGAGCTCTGACCTGACACGCGAGCTGTGACCAAGTTCTGCCACGAGA 374
 |
 QY 71 ACAGAACTCTGTGTGTCTCTCTGCGCCG 100
 |
 DB 375 ACAGAACTCTGTGTGTCTCTCTGCGCCG 404
 |

RESULT 9
 LOCUS HUMCFX 1414 bp mRNA linear PRI 01-NOV-1994
 DEFINITION Human blood-coagulation factor X mRNA, complete cds.
 ACCESSION M22613
 VERSION M22613.1 GI:180335
 KEYWORDS coagulation factor X.
 SOURCE Human liver, cDNA to mRNA, clone pKT218.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1414)
 AUTHORS Kaul,R.K., Hildebrand,B., Roberts,S. and Jagadeeswaran,P.
 TITLE Isolation and characterization of human blood-coagulation factor X cDNA
 JOURNAL Gene 41 (2-3), 311-314 (1986)
 MEDLINE 86221713

PUBMED 3011603
 FEATURES
 source
 location/Qualifiers
 1. 1414
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /map="13q34"
 1. 1414
 /gene="F10"
 <1. 1414
 /gene="F10"
 /product="coagulation factor X mRNA"
 <1. 1404
 /note="coagulation factor X precursor"
 /codon_start=1
 /protein_id="AA51984.1"
 /db_xref="GI:180336"
 /db_xref="GDB:G00-119-890"
 /translation="LIGESLIFRREOANNILARTTRANSFLEEMKKGHLRECEMEK
 SYEARREVEFSDSKTNEFNKXKDDQCEPSCONOGCKDGEYTCLEGEFEKN
 CELTTRKLSLDNGCDQFCHEONSYSCARGYTLDNGKACIPGPGCKOTLE
 RRRSVQATSSSGEAPDSITMKPYDAADLDPTENPDLDNPTOPPERDNNLTIV
 GGEVYEVYVIRKNTKRTYDPDIAVLKLPITFRMNAAPCLPERDWAESTLMT
 OKTGVSGFRTHKRGOSTRLKMLEVPYVDRNSCKLSSFTITOMNFCAGYDTKQED
 ACQDGGSPHVTFRKDYFTVGTIVSWGEGCARKGKYGITKVTAFIKWIDRSMTKRL
 PKAKSHAPEVITSSPLK"
 <1. 66
 /gene="F10"
 /note="coagulation factor X signal peptide"
 67. 483
 /gene="F10"
 /product="coagulation factor X light chain"
 493. 1401
 /gene="F10"
 /product="coagulation factor X heavy chain"
 493. 648
 /gene="F10"
 /product="coagulation factor X activation peptide"
 407 c 426 g 223 t
 BASE COUNT 358 a 407 c 426 g 223 t
 ORIGIN
 Query Match 88.4%; Score 88.4; DB 9; Length 1414;
 Best Local Similarity 98.9%; Pred. No. 3.8e-16;
 Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 AGTCACACGGAAGCTCTGACAGCTGACACAGGAGACTGTGACCACTGTCGCCACGAGA 70
 b 315 ATTACACAGGAGAGCTCTGACAGCTGACACAGGAGACTGTGACCACTGTCGCCACGAGA 374
 QY 71 ACAGAACTCTGTGTGTGCTCTGCGCCCG 100
 Db 375 ACAGAACTCTGTGTGTGCTCTGCGCCCG 404
 RESULT 10
 HUMEXM 1443 bp mRNA linear PRI 08-NOV-1994
 LOCUS Human factor X mRNA, partial signal pept and complete mature pept
 DEFINITION cds.
 ACCESSION K03194.1 GI:182840
 VERSION blood coagulation factor: factor X.
 KEYWORDS Human adult liver, cDNA to mRNA, clones pCHX[5.8,14].
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 2)
 AUTHORS Macgillivray, R.T.A.
 JOURNAL Unpublished (1985)
 REFERENCE 2 (bases 3 to 1443)
 AUTHORS Fung, M.R., Hay, C.W. and Macgillivray, R.T.
 TITLE Characterization of an almost full-length cDNA coding for human

JOURNAL blood coagulation factor X
 MEDLINE Proc. Natl. Acad. Sci. U.S.A. 82 (11), 3591-3595 (1985)
 PUBMED 85216545
 COMMENT 2582420
 During conversion of factor X to factor X-a, a glycopeptide of 52
 amino acids (encoded by positions 513-668 in this sequence) is
 released.
 A polyadenylation signal is located at position 1424-1429. This
 sequence was kindly submitted over electronic mail by
 R.T.A. Macgillivray (23-SEP-1985).
 location/Qualifiers
 1. 1443
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /map="13q34"
 1. 1443
 /gene="F10"
 <1. 1443
 /gene="F10"
 /product="X mRNA"
 1. 1433
 /partial
 /gene="F10"
 /note="factor X prepeptide"
 /codon_start=3
 /protein_id="AA52490.1"
 /db_xref="GI:182841"
 /db_xref="GDB:G00-119-890"
 /translation="SLAGLLIGESLIFRREOANNILARTTRANSFLEEMKKGHLERE
 CMEETSYEARREVEFSDSKTNEFNKXKDDQCEPSCONOGCKDGEYTCLE
 GEGKNCSELFTRKLSLDNGCDQFCHEONSYSCARGYTLDNGKACIPGPGCKOTLE
 GKOTLERRRRSVQATSSSGEAPDSITMKPYDAADLDPTENPDLDNPTOPPERDNNLTIV
 NITRTVGGCECDGECFPMQALLINENEGFCGGTILSEYITLTAHCLYQAKRFRVRY
 GDRNTEOEGEGEVAHEVEVYIKHNRTKRTYDPDIAVLKLPITFRMNAAPCLPER
 DWAESTLMTOKTGVSGFRTHKRGOSTRLKMLEVPYVDRNSCKLSSFTITOMNFC
 AGYDTKQEDACQDGGSPHVTFRKDYFTVGTIVSWGEGCARKGKYGITKVTAFIKWID
 RSMKTRGLPKAKSHAPEVITSSPLK"
 <1. 86
 /gen="F10"
 /note="factor X signal peptide"
 87. 503
 /gene="F10"
 /product="factor X light chain"
 513. 1430
 /gene="F10"
 /product="factor X heavy chain"
 1117
 /gene="F10"
 /note="a in pCHX8; t in pCHX5"
 416 c 435 g 231 t
 BASE COUNT 361 a 416 c 435 g 231 t
 ORIGIN
 Query Match 88.4%; Score 88.4; DB 9; Length 1443;
 Best Local Similarity 98.9%; Pred. No. 3.8e-16;
 Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 AGTCACACGGAAGCTCTGACAGCTGACACAGGAGACTGTGACCACTGTCGCCACGAGA 70
 Db 335 ATTACACAGGAGAGCTCTGACAGCTGACACAGGAGACTGTGACCACTGTCGCCACGAGA 394
 QY 71 ACAGAACTCTGTGTGTGCTCTGCGCCCG 100
 Db 395 ACAGAACTCTGTGTGTGCTCTGCGCCCG 424
 RESULT 11
 LOCUS A86859 1467 bp DNA linear PAT 22-JAN-2000
 DEFINITION Sequence 43 from Patent M09838318.
 ACCESSION A86859
 VERSION A86859.1 GI:6735650
 KEYWORDS
 SOURCE unidentified.

ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1467)
AUTHORS Falkner, F. and Himmelspach, M.
TITLE FACTOR X DELETION MUTANTS AND ANALOGUES THEREOF
JOURNAL Patent: WO 9838317-A 43 03-SEP-1998;
FALKNER FALKO GUENTER (AT); HIMMELSPACH MICHELE (AT)
FEATURES
source
1. 1467
/organism="unclassified"
/db_xref="taxon:32644"
1. 1467
/note="unnamed protein product"
/codon_start=1
/protein_id="CAB69367.1"
/db_xref="GI:6735651"
/translation="MGRLPLHLVLSASLACLLLGESLFTIREQANNILARYTRANSP
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GKACIPGPPGCKQTLERKRSVAQATSSGAPSIYKPYDADLDPTENPDL
DFNOTPERGDNMLTRIVGGECKDGSCPMQALLINBENEGCGGTLISFEYITTAH
CLYOKRFKRVGDRNTEOEGEAEV IEEVYVVKHNRFTETIDPDIAYLRKTPTE
RMVAPACLPDERMAESTLMTOKTGI /SGGRT/IEKROSTF/KMLEVYVDNNSKL
SSSFITONMFCAGYDTKODACOGD /GGPHVTRFDYFVTGIVSWGSCAKKRYG
LYKVTAFKMWIDRSMTKRLGPKAKSHAPEVITSSPLK"

BASE COUNT 363 a 424 c 444 g 236 t
ORIGIN

Query Match 88.4%; Score 88.4; DB 6; Length 1467;
Best Local Similarity 98.9%; Pred. No. 3.8e-16;
Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 11 AGTCACAGGAAGCTCTGCAGCTGACCAACGGGAGCTGTGACCAAGTTCGCCACGAGA 70
DB 369 ATTACACAGGAAGCTCTGCAGCTGACCAACGGGAGCTGTGACCAAGTTCGCCACGAGA 428
OY 71 ACAGAACTCTGTGTGCTGCTCTGCCGCCG 100
DB 429 ACAGAACTCTGTGTGCTGCTGCCGCCG 458

RESULT 12
LOCUS A86886 1467 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 26 from Patent W09838317.
ACCESSION A86886
VERSION A86886.1 GI:6735677
KEYWORDS
UNCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1467)
AUTHORS Himmelspach, M. and Eibl, J.
TITLE FACTOR X ANALOGUES WITH A MODIFIED PROTEASE CLEAVAGE SITE
JOURNAL Patent: WO 9838317-A 26 03-SEP-1998;
HIMMELSPACH MICHELE (AT); EIBL JOHANN (AT)
FEATURES
source
1. 1467
/organism="unclassified"
/db_xref="taxon:32644"
1. 1467
/note="unnamed protein product"
/codon_start=1
/protein_id="CAB69368.1"
/db_xref="GI:6735678"
/translation="MGRLPLHLVLSASLACLLLGESLFTIREQANNILARYTRANSP
LEMKKGLHERBCEMEETCSYEAREVEDDKNEFNWNYKDGDETSFCOMGRCK
DGLGEYTCCTLEGEKNCLEFTRKLSLNGDCDOFCHEONSVCSCARGYTLADN
GKACIPGPPGCKQTLERKRSVAQATSSGAPSIYKPYDADLDPTENPDL
DFNOTPERGDNMLTRIVGGECKDGSCPMQALLINBENEGCGGTLISFEYITTAH
CLYOKRFKRVGDRNTEOEGEAEV IEEVYVVKHNRFTETIDPDIAYLRKTPTE
RMVAPACLPDERMAESTLMTOKTGI /SGGRT/IEKROSTF/KMLEVYVDNNSKL
SSSFITONMFCAGYDTKODACOGD /GGPHVTRFDYFVTGIVSWGSCAKKRYG
LYKVTAFKMWIDRSMTKRLGPKAKSHAPEVITSSPLK"

BASE COUNT 363 a 424 c 444 g 236 t
ORIGIN

Query Match 88.4%; Score 88.4; DB 6; Length 1467;
Best Local Similarity 98.9%; Pred. No. 3.8e-16;
Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 11 AGTCACAGGAAGCTCTGCAGCTGACCAACGGGAGCTGTGACCAAGTTCGCCACGAGA 70
DB 369 ATTACACAGGAAGCTCTGCAGCTGACCAACGGGAGCTGTGACCAAGTTCGCCACGAGA 428
OY 71 ACAGAACTCTGTGTGCTGCTCTGCCGCCG 100
DB 429 ACAGAACTCTGTGTGCTGCTGCCGCCG 458

RESULT 13
LOCUS AX082959 1467 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 1 from Patent W00110896.
ACCESSION AX082959
VERSION AX082959.1 GI:13184880
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1467)
AUTHORS Himmelspach, M. and Schlokat, U.
TITLE Factor x analog with an improved ability to be activated
JOURNAL Patent: WO 0110896-A 1 15-FEB-2001;
Baxter Aktiengesellschaft (AT)
FEATURES
source
1. 1467
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 363 a 424 c 444 g 236 t
ORIGIN

Query Match 8.4%; Score 88.4; DB 6; Length 1467;
Best Local Similarity >8.9%; Pred. No. 3.8e-16;
Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 11 AGTCACAGGAAGCTCTGCAGCTGACCAACGGGAGCTGTGACCAAGTTCGCCACGAGA 70
DB 369 ATTACACAGGAAGCTCTGCAGCTGACCAACGGGAGCTGTGACCAAGTTCGCCACGAGA 428
OY 71 ACAGAACTCTGTGTGCTGCTCTGCCGCCG 100
DB 429 ACAGAACTCTGTGTGCTGCTGCCGCCG 458

RESULT 14
LOCUS AR024194 1500 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 4 from patent US 5795863.
ACCESSION AR024194
VERSION AR024194.1 GI:3977488
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 1500)
AUTHORS Wolf, D.
TITLE Recombinant agents affecting thrombosis
JOURNAL Patent: US 5795863-A 4 18-AUG-1998;
FEATURES
source
1. 1500
/organism="unknown"

BASE COUNT 390 a 425 c 441 g 244 t
ORIGIN

Query Match 88.4%; Score 88.4; DB 6; Length 1500;
Best Local Similarity 98.9%; Pred. No. 3.8e-16;
Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 401 ATTACACAGGAGCTCTGACCTGACACAGGAGCTGTGACCATTTCTGCACGAGA 460
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QY 71 ACAGAACTCTGTGTGTCTGCTGCGCCCG 100
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DB 461 ACAGAACTCTGTGTGTCTGCTGCGCCCG 490
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RESULT 15

HUMFACX

LOCUS HUMFACX 1507 bp mRNA linear PRI 08-NOV-1994
DEFINITION Human coagulation factor X (F10) mRNA, complete cds.
ACCESSION M57285
VERSION M57285.1 GI:182389
KEYWORDS coagulation factor X.
SOURCE Human, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS Messier, T.L., Pittman, D.D., Long, G.L., Kaufman, R.J. and Church, W.R.
TITLE 1 (bases 1 to 1507)
JOURNAL Cloning and expression in COS-1 cells of a full-length cDNA
MEDLINE Gene 99 (2), 291-294 (1991)
PUBMED 91216473
FEATURES 1902434

FEATURES
source location/Qualifiers

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/map="13q34"
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/db_xref="GDB:600-119-890"

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DENOTOPERGDNNLFRIVGGCKKQCEPQWALLINENEGFCGTTLSSEYILTAH
CLYQAKRFKRVVDRNTBOEGEGDAVHEVYIKHNRFTKETEDDIATLRLKPTTF
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BASE COUNT 394 a 429 c 446 g 238 t
ORIGIN

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Best Local Similarity 98.9%; Pred. No. 3.8e-16;
Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 AGTCACAGGAGCTCTGACCTGACACAGGAGCTGTGACCATTTCTGCACGAGA 70
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DB 369 ATTACACAGGAGCTCTGACCTGACACAGGAGCTGTGACCATTTCTGCACGAGA 428
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QY 71 ACAGAACTCTGTGTGTCTGCTGCGCCCG 100
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DB 429 ACAGAACTCTGTGTGTGTGTGTCTGCGCCCG 458
Search completed: January 15, 2003, 20:35:16
Job time: 1355 secs

GenCore version 5.1.
Copyright (c) 1993 - 2003 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: January 15, 2003, 17:58:10 : Search time 31 Seconds

(without alignments)
989.280 Million cell updates/sec

Title: L00394_COPY_1_100

Perfect score: 1 CTCCTTGGCAGTCACACG.....GTGGTGTGCTCTGCGCCG 100

Sequence: IDENTITY NUC

Scoring table: Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_MN:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	88.4	88.4	1126	3	US-08-487-427-27
3	88.4	88.4	1126	3	US-08-479-727A-27
4	88.4	88.4	1126	3	US-08-482-369A-27
5	88.4	88.4	1126	5	PCT-US95-07439-27
6	88.4	88.4	1404	4	US-09-202-101-15
7	88.4	88.4	1500	1	US-08-487-037-1
8	52.4	52.4	1554	1	US-08-469-486-1
9	52.4	52.4	1554	2	US-08-469-658-1
10	30.8	30.8	2451	1	US-08-282-141-1
11	28.2	28.2	22306	4	US-09-453-702B-251
12	28.2	28.2	46819	4	US-09-453-702B-72
13	26.8	26.8	4403765	4	US-09-103-840A-2
14	26.8	26.8	4411529	4	US-09-103-840A-1
15	26.4	26.4	3156	4	US-09-284-819-8
16	25.8	25.8	10095	3	US-08-822-586-45
17	25.4	25.4	286	2	US-08-675-508-21
18	25.4	25.4	1409	4	US-09-338-907-72
19	25.4	25.4	1409	4	US-09-338-907-72
20	25.4	25.4	1409	4	US-09-218-207-72
21	25.4	25.4	1409	4	US-09-218-207-184
22	25.4	25.4	4550	4	US-09-338-907-182
23	25.4	25.4	4550	4	US-09-218-207-182
24	25.2	25.2	1866	4	US-09-615-192A-103
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26	25.2	25.2	6677	4	US-08-939-366-27
27	25.2	25.2	6677	4	US-09-467-997-6

28	25.2	25.2	10079	2	US-08-476-866-20	Sequence 20, Appl
29	25	25.0	1386	2	US-08-756-506-3	Sequence 3, Appl
30	25	25.0	1387	6	5270178-1	Patent No. 5270178
31	25	25.0	1755	6	522537-1	Patent No. 522537
32	25	25.0	2373	4	US-08-980-080-1	Sequence 1, Appl
33	25	25.0	3003	1	US-08-434-730-15	Sequence 15, Appl
34	25	25.0	4493	4	US-09-417-822-6	Sequence 4, Appl
35	25	25.0	4534	4	US-09-417-822-7	Sequence 7, Appl
36	25	25.0	4535	4	US-09-417-822-8	Sequence 8, Appl
37	25	25.0	8838	4	US-09-417-822-1	Sequence 1, Appl
38	25	25.0	11725	2	US-08-756-506-1	Sequence 1, Appl
39	24.8	24.8	288	2	US-08-675-508-23	Sequence 23, Appl
40	24.8	24.8	494	2	US-08-675-508-4	Sequence 4, Appl
41	24.8	24.8	998	4	US-09-203-939-1	Sequence 1, Appl
42	24.8	24.8	998	4	US-09-251-835-1	Sequence 1, Appl
43	24.8	24.8	998	4	US-09-318-503-1	Sequence 1, Appl
44	24.8	24.8	998	4	US-09-038-261A-1	Sequence 1, Appl
45	24.8	24.8	1485	4	US-09-088-435-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-479-733A-27
Sequence 27, Application US/08479733A
Patent No. 5877289
GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: Edgington, Thomas S.
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Specific Coagulation of Vasculature
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,733A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/273,567
FILING DATE: 11-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/418-3000
TELEX: N/A
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1126 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-479-733A-27
Query Match 88.4% Score 88.4: DB 2: Length 1126:
Best local similarity 98.9% Pred. No. 1e-19:
Matches 89: Conservative 0: Mismatches 1: Indels 0: Gaps 0:
QY 11 AGTCACGAGGAGCTGTGACGCTGTGACGAGGAGCTGTGACGAGGAGGAGA 70

Db 27 ATTACACGAGGAGCTGCGACCTGGACAAAGGGGAGCTGTGACCAAGTTGCGCCAGAGGA 86
QY 71 ACAGAACTCTGTGTGCTGCTGCTGCGCCG 100
Db 87 ACAGAACTCTGTGTGCTGCTGCTGCGCCG 116

RESULT 2

US-08-487-427-27
Sequence 27, Application US/08487427
Patent No. 6004555

GENERAL INFORMATION:

APPLICANT: Thorpe, Phillip E.
APPLICANT: Edgington, Thomas S.
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Specific Coagulation of Vasculature
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,427
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/273,567
FILING DATE: 11-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:457/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
TELEX: N/A

SEQUENCE CHARACTERISTICS:
LENGTH: 1126 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-487-427-27

Query Match 88.4%; Score 88.4; DB 3; Length 1126;
Best Local Similarity 98.9%; Pred. No. 1e-19;
Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 27 ATTACACGAGGAGCTGTGACCTGGACAAAGGGGAGCTGTGACCAAGTTGCGCCAGAGGA 86

QY 71 ACAGAACTCTGTGTGCTGCTGCTGCGCCG 100
Db 87 ACAGAACTCTGTGTGCTGCTGCTGCGCCG 116

RESULT 3

US-08-479-727A-27
Sequence 27, Application US/08479727A
Patent No. 6036955

GENERAL INFORMATION:
APPLICANT: Thorpe, Phillip E.
TITLE OF INVENTION: Methods and Compositions for the

TITLE OF INVENTION: Specific Coagulation of Vasculature
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,727A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/273,567
FILING DATE: 11-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:461/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
TELEX: N/A

SEQUENCE CHARACTERISTICS:
LENGTH: 1126 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-479-727A-27

Query Match 88.4%; Score 88.4; DB 3; Length 1126;
Best Local Similarity 98.9%; Pred. No. 1e-19;
Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 27 ATTACACGAGGAGCTGTGACCTGGACAAAGGGGAGCTGTGACCAAGTTGCGCCAGAGGA 86

QY 71 ACAGAACTCTGTGTGCTGCTGCTGCGCCG 100
Db 87 ACAGAACTCTGTGTGCTGCTGCTGCGCCG 116

RESULT 4

US-08-482-369A-27
Sequence 27, Application US/08482369A
Patent No. 6093399

GENERAL INFORMATION:

APPLICANT: Thorpe, Phillip E.
APPLICANT: Edgington, Thomas S.
TITLE OF INVENTION: Methods and Compositions for the Specific
TITLE OF INVENTION: Coagulation of Vasculature
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,369A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/273,567
FILING DATE: 11-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: USFD433P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1126 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

Query Match 88.4%; Score 88.4; DB 3; Length 1126;
Best Local Similarity 98.9%; Pred. No. 1e-19; Indels 1; Gaps 0;
Matches 89; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

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DB 27 ATTCAACGGAGAGCTGTGACCTGACCAACGGGAGCTGTGACCACTTCTGCCACGAGGA 86
QY 71 ACAGAACTCTGTGTGTGCTCTCTGCGCCG 100
DB 87 ACAGAACTCTGTGTGTGCTCTCTGCGCCG 116

RESULT 5
PCT-US95-07439-27
Sequence 27, Application PC/TUS9507439
GENERAL INFORMATION:

APPLICANT: BOARD OF REGENTS, THE UNIVERSITY OF
APPLICANT: TEXAS SYSTEM
APPLICANT: STREET: 201 West 7th Street
APPLICANT: CITY: Austin
APPLICANT: STATE: Texas
APPLICANT: COUNTRY: United States of America
APPLICANT: POSTAL CODE: 78701
APPLICANT: TELEPHONE NO: (512)499-4462
APPLICANT: TELEFAX: (512)499-4523
APPLICANT: NAME: THE SCRIPPS RESEARCH INSTITUTE
APPLICANT: STREET: 10666 North Torrey Pines Road
APPLICANT: CITY: La Jolla
APPLICANT: STATE: California
APPLICANT: COUNTRY: United States of America
APPLICANT: POSTAL CODE: 92037
TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: FOR THE SPECIFIC
TITLE OF INVENTION: COAGULATION OF VASCULATURE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07439
FILING DATE: Concurrently herewith

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/273,567
FILING DATE: 11-JUN 1994
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: USFD433P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1126 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

Query Match 88.4%; Score 88.4; DB 5; Length 1126;
Best Local Similarity 98.9%; Pred. No. 1e-19; Indels 1; Gaps 0;
Matches 89; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 11 AGTACACGGAGAGCTGTGACCTGACCAACGGGAGCTGTGACCACTTCTGCCACGAGGA 70
DB 27 ATTCAACGGAGAGCTGTGACCTGACCAACGGGAGCTGTGACCACTTCTGCCACGAGGA 86
QY 71 ACAGAACTCTGTGTGTGCTCTCTGCGCCG 100
DB 87 ACAGAACTCTGTGTGTGCTCTCTGCGCCG 116

RESULT 6
US-09-202-101-15
Sequence 15, Application US/09202101
Patent No. 6277618
GENERAL INFORMATION:

APPLICANT: Recombinant blood-coagulation proteases
TITLE OF INVENTION: 17
NUMBER OF SEQUENCES: 17
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30B (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/202,101
FILING DATE:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-202-101-15

Query Match 88.4%; Score 88.4; DB 4; Length 1404;
Best Local Similarity 98.9%; Pred. No. 1e-19; Indels 1; Gaps 0;
Matches 89; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 11 AGTACACGGAGAGCTGTGACCTGACCAACGGGAGCTGTGACCACTTCTGCCACGAGGA 70
DB 315 ATTCAACGGAGAGCTGTGACCTGACCAACGGGAGCTGTGACCACTTCTGCCACGAGGA 374
QY 71 ACAGAACTCTGTGTGTGCTCTCTGCGCCG 100
DB 375 ACAGAACTCTGTGTGTGCTCTCTGCGCCG 404

RESULT 7
US-08-487-037-4

US-08-469-658-1
Sequence 1, Application US/08469658
Patent No. 5917018
GENERAL INFORMATION:
APPLICANT: Th egeresen, Hans Christian
APPLICANT: Hollet, Thor Ias
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOOLDING OF
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
#1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,658
FILING DATE: June 5, 1995

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: TYPE: nucleic acid
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: cDNA
US-08-282-141-1

Query Match
Best Local Similarity 30.8%; Score 30.8; DB 1; Length 2461;
Matches 47; Conservative 0; Mismatches 27; Indels 0; Gaps 0

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QY 87 TGCTCTGGCGCCG 100
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DB 672 TGTTCTGCCACAG 685

RESULT 11
US-09-453-702B-251
: Sequence 251, Application US/09453702B
: Patent No. 6365723
: GENERAL INFORMATION:
: APPLICANT: Blattner, Frederick R.
: Burland, Valerie
: Perna, Nicole T.
: Plunkett, Guy
: Welch, Rod
: TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
: NUMBER OF SEQUENCES: 265
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Quarles & Brady
: STREET: 1 South Plinckney Street
: CITY: Madison
: STATE: WI
: COUNTRY: US
: ZIP: 53701-2113
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Word Perfect 8.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/453,702B
: FILING DATE: 03-Dec-1999
: CLASSIFICATION: <unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/110,955
: FILING DATE: 04-DEC-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Seay, Nicholas J.
: REGISTRATION NUMBER: 27386
: REFERENCE/DOCKET NUMBER: 960296.95017
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (608) 251-5000
: TELEFAX: (608) 251-9166
: INFORMATION FOR SEQ ID NO: 251:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 22306
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: SEQUENCE DESCRIPTION: SEQ ID NO: 251:
US-09-453-702B-251

Query Match
Best Local Similarity 28.2%; Score 28.2; DB 4; Length 22306;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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Db 16880 CTGATGCGCTTCGGGCTGACCATCCGAACTGTCTCCGGAACAGTCGCGAGGAGCGGTA 16939
 QY 78 TCTGTGTTGTGCT 90
 Db 16940 TCCGAGGTGGCT 16952

RESULT 12
 US-09-453-702B-72/c
 ; Sequence 72, Application US/09453702B
 ; Patent No. 6365723
 ; GENERAL INFORMATION:
 APPLICANT: Blatner, Frederick R.
 Burland, Valerie
 Perna, Nicole T.
 Plunkett, Guy
 Welch, Rod

TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Quarles & Brady
 STREET: 1 South Plinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/453,702B
 FILING DATE: 03-Dec-1999
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/110,955
 FILING DATE: 04-DEC-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27386
 REFERENCE/DOCKET NUMBER: 960296.95017

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (608) 251-5000
 TELEFAX: (608) 251-9166
 INFORMATION FOR SEQ ID NO: 72:

SEQUENCE CHARACTERISTICS:
 LENGTH: 46819
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 72:
 US-09-453-702B-72

Query Match 28.2%; Score 28.2; DB 4; Length 46819;
 Best Local Similarity 61.6%; Pred. No. 6.3; Mismatches 28; Indels 0; Gaps 0;

QY 18 CGGAAGCTCTGAGCCTGACACAGGGGAGTGTGACCACTTGTCCACGAGAGACAGAAC 77
 Db 15108 CTGATGCGCTTCGGGCTGCATCCGGAACGTGTCTCCGGAACAGTCGCGAGGAGCGGTA 15049
 QY 78 TCTGTGTTGTGCT 90
 Db 15048 TCCGAGGTGGCT 15036

RESULT 13
 US-09-103-840A-2/c
 ; Sequence 2, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:

APPLICANT: FLEISCHMAN, Robert D.
 APPLICANT: WHITE, Owen R.
 APPLICANT: FRASER, Claire M.
 APPLICANT: VENTER, John C.
 TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 TITLE OF INVENTION: TUBERCULOSIS
 FILE REFERENCE: 24366-20007.00
 CURRENT APPLICATION NUMBER: US/09/103,840A
 CURRENT FILING DATE: 1998-06-24
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2
 LENGTH: 4403765
 TYPE: DNA
 ORGANISM: Mycobacterium tuberculosis
 FEATURE:
 OTHER INFORMATION: CDC 1551
 OTHER INFORMATION: "n" bases at various positions throughout the sequence
 OTHER INFORMATION: represent a, t, c or g
 US-09-103-840A-2

Query Match 26.8%; Score 26.8; DB 4; Length 4403765;
 Best Local Similarity 68.5%; Pred. No. 38;
 Matches 37; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 6 TTGGCAGTCACACGAGAGCTCTGACAGCTGACAGCGGGAGTGTGACCACTTC 59
 Db 3915983 TTGGGAATCGCACCGGATATCTTGACCTGACGACGACGAGCTATGCGCTGTC 3915930

RESULT 14
 US-09-103-840A-1/c
 ; Sequence 1, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:

APPLICANT: FLEISCHMAN, Robert D.
 APPLICANT: WHITE, Owen R.
 APPLICANT: FRASER, Claire M.
 APPLICANT: VENTER, John C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 TITLE OF INVENTION: TUBERCULOSIS
 FILE REFERENCE: 24366-20007.00
 CURRENT APPLICATION NUMBER: US/09/103,840A
 CURRENT FILING DATE: 1998-06-24
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 4411529
 TYPE: DNA
 ORGANISM: Mycobacterium tuberculosis
 OTHER INFORMATION: H37RV
 US-09-103-840A-1

Query Match 26.8%; Score 26.8; DB 4; Length 4411529;
 Best Local Similarity 68.5%; Pred. No. 38;
 Matches 37; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 6 TTGGCAGTCACACGAGAGCTCTGACAGCTGACAGCGGGAGTGTGACCACTTC 59
 Db 3922204 TTGGGAATCGCACCGGATATCTTGACCTGACGACGACGAGCTATGCGCTGTC 3922151

RESULT 15
 US-09-284-819-8/c
 ; Sequence 8, Application US/09284819
 ; Patent No. 6365712
 ; GENERAL INFORMATION:
 APPLICANT: Kelly, Kathleen
 APPLICANT: The Government of the United States of America
 APPLICANT: as represented by The Secretary of the
 APPLICANT: Department of Health and Human Services
 TITLE OF INVENTION: Methods and Compositions for Inhibiting Inflammation
 TITLE OF INVENTION: and Angiogenesis Comprising a Mammalian CD97 Alpha

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2003, 20:35:40 : Search time 32.5 Seconds
(without alignments)
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Title: L00396_COPY_1_100
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Sequence: 1

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 393868 seqs, 222934149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36.0	1047	9	US-09-808-602-100	Sequence 100, App
2	34.2	1795	9	US-09-764-898-72	Sequence 72, App
3	34.2	2063	9	US-10-063-547-111	Sequence 111, App
4	34.2	2063	9	US-10-174-590-329	Sequence 329, App
5	34.2	2063	9	US-10-176-758-329	Sequence 329, App
6	34.2	2063	12	US-10-006-867-111	Sequence 111, App
7	34.2	2063	12	US-10-052-86-329	Sequence 329, App
8	34.2	2079	10	US-09-851-588-5	Sequence 5, App
9	34.2	2081	10	US-09-851-588-7	Sequence 7, App
10	30.2	396	10	US-09-960-352-10052	Sequence 10052, App
11	30.2	420	10	US-09-960-352-6361	Sequence 6361, App
12	29.8	1674	9	US-09-738-626-1340	Sequence 1340, App
13	29.6	1059	10	US-09-888-615-36	Sequence 36, App
14	28.4	1047	10	US-09-755-016-5	Sequence 5, App
15	28.4	1047	10	US-09-755-016-3	Sequence 3, App
16	28.4	1080	10	US-09-888-615-55	Sequence 55, App
17	28.4	1286	10	US-09-755-016-7	Sequence 7, App
18	28.4	424	10	US-09-960-352-5863	Sequence 5863, App
19	28.0	1383	10	US-09-841-880-3	Sequence 3, App

20	28.0	1413	10	US-09-884-901-2	Sequence 2, App
21	28.0	1548	10	US-09-150-811-6	Sequence 6, App
22	28.0	1937	10	US-09-841-880-1	Sequence 1, App
23	28.0	2792	10	US-09-118-748-1	Sequence 1, App
24	28.0	32187	10	US-09-764-847-1550	Sequence 1550, App
25	28.0	32193	10	US-09-764-847-1549	Sequence 1549, App
26	28.0	38059	10	US-09-880-107-2125	Sequence 2125, App
27	27.8	3286	9	US-10-013-310-4	Sequence 4, App
28	26.8	857	10	US-09-822-849A-158	Sequence 158, App
29	26.6	224	10	US-09-728-446-1164	Sequence 1164, App
30	26.6	26.6	10	US-09-888-615-32	Sequence 32, App
31	26.6	1543	10	US-09-917-800A-1575	Sequence 1575, App
32	26.4	26.4	9	US-09-147-947-5	Sequence 5, App
33	26.4	26.4	9	US-09-147-947-3	Sequence 3, App
34	26.2	1839	10	US-09-950-294-3	Sequence 3, App
35	26.2	26.2	9	US-10-047-542-12	Sequence 12, App
36	26.2	26.2	9	US-09-982-107-3	Sequence 3, App
37	26.2	2919	9	US-09-989-919-74	Sequence 74, App
38	26.2	3149	9	US-09-981-353-58	Sequence 58, App
39	26.2	7129	9	US-10-047-542-101	Sequence 101, App
40	26.2	8074	9	US-10-047-542-14	Sequence 14, App
41	26.0	681	9	US-10-078-770-91	Sequence 91, App
42	25.8	2063	10	US-09-925-302-169	Sequence 169, App
43	25.8	2386	9	US-09-808-602-92	Sequence 92, App
44	25.8	2493	10	US-09-880-107-2256	Sequence 2256, App
45	25.8	2555	12	US-10-044-090-613	Sequence 613, App

ALIGNMENTS

RESULT 1
US-09-808-602-100
Sequence 100, Application US/09808602
Patent No. US2002015115A1
GENERAL INFORMATION:
APPLICANT: Vernet, Corine A
APPLICANT: Shinkets, Richard A
APPLICANT: Herrman, John L
APPLICANT: Majumder, Kumud
APPLICANT: Mishra, Vishnu
APPLICANT: Mezes, Peter S
APPLICANT: Macdonald, John
TITLE OF INVENTION: No. US2002015115A1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 1566-697 CIP
CURRENT APPLICATION NUMBER: US/09/808, 602
PRIORITY FILING DATE: 2001-03-14
PRIORITY APPLICATION NUMBER: 09/800, 198
PRIORITY FILING DATE: 2001-03-05
PRIORITY APPLICATION NUMBER: 60/186, 596
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 100
LENGTH: 1047
TYPE: DNA
ORGANISM: Homo sapiens
US-09-808-602-100
Query Match
Best Local Similarity 64.3%: Pred. 0.00054:
Matches 54; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
OY 17 TCGTCATGATGAGAAACGAGGCTTCTGTGTGAGAACATTTCTGAGCGAGTTCTTACA 76
DB 207 TGAGCATTCAGGAAGTAGACACCATTTCTGTGGGGGCTCATTTCTGAGTGTGTGGA 266
OY 77 TCGTACCGGACGACGACGCTCTCT 100
DB 267 TCGTCACCGTGGCCGACGCTCTCT 290

OY 21 CATCAATGAGGAAACAGAGGTTCTGTGTGAACCATCTTGAGCGAGTTTACATCCT 80
 Db 857 CATCCAGTACGACAAACAGCAGCTGTGTGAGGAGCATCCTGACCCCACTGGTCTCT 916
 OY 81 AACGGCAGCCCACTGTCTC 99
 Db 917 CACGGCAGCCCACTGTCTC 935

RESULT 6
 US-10-006-867-111
 ; Sequence 111, Application US/10006867
 ; Patent No. US20020119130A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Geriltsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Matanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/006,867
 ; PRIOR FILING DATE: 2001-12-06
 ; PRIOR APPLICATION NUMBER: 60/063435
 ; PRIOR FILING DATE: 1997-10-29
 ; PRIOR APPLICATION NUMBER: 60/064215
 ; PRIOR FILING DATE: 1997-10-29
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PRIOR FILING DATE: 1998-06-12
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PRIOR FILING DATE: 1998-06-16
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PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
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PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089908

Query Match 34.2% Score 34.2; DB 12; Length 2063;
Best Local Similarity 64.6%; Pred. No. 0.0034;
Matches 51; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 21 CATCATGAGGAAAGAGAGGTTCTGTGTCGGAACCATTCGAGGAGTTTACATCCT 80
DB 857 CATCCAGTACGACAAACACACGCTGTGTGAGGAGCATCTCGACCCCACTGGTCTCT 916
QY 81 AACGGAGCCCACTGTCTC 99

Db 29 TCCTTTTCATGTTGGAATTCGATCTGTGGAGGTTCCATCTTAATGAAAAATGG 88
OY 77 TCCTAACGAGCCGACTGTC 99
Db 89 TTGTAAGTGCAGCCGACTGCATC 111

RESULT 12
US-09-738-626-1340/C

Sequence 1340, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 1340
LENGTH: 1674
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-1340

Query Match 29.8%; Score 29.8; DB 9; Length 1674;
Best Local Similarity 66.2%; Pred. No. 0.14;
Matches 43; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

OY 13 GCCCTGCTATCAATGAGAAACGAGGGTTCTGTGTCGATCCATTCTGAGCGAGTTC 72
Db 714 GCCCTGCTCTCTCGAGGCTCTTACGACGAGGCTGCAATGTTGAGCCCTCTGACCGATTGC 655
73 TACAT 77
Db 654 GACGT 650

RESULT 13
US-09-888-615-36

Sequence 36, Application US/09888615
Patent No. US20020064856A1
GENERAL INFORMATION:

APPLICANT: PLOWMAN, GREGORY
APPLICANT: WHITE, DAVID
APPLICANT: CAENEPEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: MANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 36
LENGTH: 1059
TYPE: DNA
ORGANISM: Homo sapiens
US-09-888-615-36

Query Match 29.6%; Score 29.6; DB 10; Length 1059;
Best Local Similarity 64.7%; Pred. No. 0.14;
Matches 44; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 33 AAACGAGGTTTCTGTGTCGATCCATTCTGAGCGAGTTCATCTTAAGCGGACCCCA 92

Db 264 AAGTGAACCTTCTGTGCGGCTCATCTCAACAGTGTGATTCATCTGCGGCTCA 323

OY 93 CTGCTCTCT 100
Db 324 CTGCTTAT 331

RESULT 14
US-09-755-016-5

Sequence 5, Application US/09755016
Patent No. US20010034437A1
GENERAL INFORMATION:

APPLICANT: WAIKE, D. Wade
APPLICANT: WILGANSKI, Nathaniel L.
APPLICANT: Donoho, Gregory
TITLE OF INVENTION: No. US20010034437A1 Human Proteases and Polynucleotides Enc
FILE REFERENCE: LEX-0114-USA
CURRENT APPLICATION NUMBER: US/09/755,016
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/174,686
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 867
TYPE: DNA
ORGANISM: Homo sapien
US-09-755-016-5

Query Match 28.4%; Score 28.4; DB 10; Length 867;
Best Local Similarity 70.4%; Pred. No. 0.36;
Matches 38; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 42 TTTCTGTGTCGAGAACCATCTTGAGCGAGTTCATCTTAAGCGGACCCACTG 95
Db 135 TGTATGTGGGGAACCCCTAGTAGAGAGAGGTGGTCTCTCAACAGCTGCCACTG 188

RESULT 15
US-09-755-016-3

Sequence 3, Application US/09755016
Patent No. US20010034437A1
GENERAL INFORMATION:

APPLICANT: WAIKE, D. Wade
APPLICANT: WILGANSKI, Nathaniel L.
APPLICANT: Donoho, Gregory
TITLE OF INVENTION: No. US20010034437A1 Human Proteases and Polynucleotides Enc
FILE REFERENCE: LEX-0114-USA
CURRENT APPLICATION NUMBER: US/09/755,016
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/174,686
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1047
TYPE: DNA
ORGANISM: Homo sapien
US-09-755-016-3

Query Match	28.4%	Score 28.4	DB 10	Length 1047
Best Local Similarity	70.4%	Pred. No. 0.39		
Matches	38	Conservative	0	Mismatches 16; Indels 0; Gaps 0;
0y	42	TTCTGTTGATGGAACATTCTAGAGGAGTTCACACTTCACAGGAGGACCATG	95	
	1			
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Search completed: January 15, 2003, 22:32:23
Job time : 34.5 secs

enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com>

BASE COUNT 129 a 263 c 250 g 210 t 3 others

Query Match 92.6%; Score 92.6; DB 9; Length 855;
Best Local Similarity 96.0%; Pred. No. 3.7e-22;
Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTCGTACAGAGCCCTGCTCATCATGAGAAAGAGGTTTCTGTGGGAGCACTTC 61
DB 672 GTCCCTGACAGCCCTGCTCATCATGAGAAAGAGGTTTCTGTGGGAGCACTTC 613
QY 62 TGAGCGAGTTCTACATCTTAACGCGAGCCCACTGTCTCT 100
612 TGAGCGAGTTCTACATCTTAACGCGAGCCCACTGTCTCT 574

RESULT 2
AL576464/c 806 bp mRNA linear EST 16-FEB-2001
LOCUS AL576464 LTI_NFL006_PL2 Homo sapiens cDNA clone CSOD1076YA10 3
DEFINITION AL576464 prime, mRNA sequence.
ACCESSION AL576464
VERSION AL576464.1 GI:12938633
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 806)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polyes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: secref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source location/Qualifiers

1..806
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSOD1076YA10"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com>"

BASE COUNT 124 a 251 c 239 g 188 t 4 others

Query Match 92.2%; Score 92.2; DB 9; Length 806;
Best Local Similarity 94.9%; Pred. No. 4.9e-22;
Matches 94; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTCGTACAGAGCCCTGCTCATCATGAGAAAGAGGTTTCTGTGGGAGCACTTC 61
DB 692 GTCCCTGACAGCCCTGCTCATCATGAGAAAGAGGTTTCTGTGGGAGCACTTC 633
QY 62 TGAGCGAGTTCTACATCTTAACGCGAGCCCACTGTCTCT 100

DB 632 TGAGCGAGTTCTACATCTTAACGCGAGCCCACTGTCTCT 594

RESULT 3
BE766639 246 bp mRNA linear EST 19-SEP-2000
LOCUS IL3-NT0105-200700-220-A03 NT0105 Homo sapiens cDNA, mRNA sequence.
DEFINITION BE766639.1 GI:10196563
ACCESSION BE766639
VERSION BE766639.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 246)
AUTHORS Dias Neto, E., Garcia Correa, R., Verlovski-Almeida, S., Brites, M.R., Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be found in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l=62-IL3-NT0105-200700-220-A03&t3=2000-07-20&t4=1>)
Seq primer: puc 18 forward
High quality seq. nce stop: 246.

FEATURES
source location/Qualifiers

1..246
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0105"
/dev_stage="Adult"
/note="Organ: nervous-tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 59 a 70 c 73 g 44 t

Query Match 91.0%; Score 91; DB 12; Length 246;
Best Local Similarity 94.9%; Pred. No. 6.8e-22;
Matches 94; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GTCGTACAGAGCCCTGCTCATCATGAGAAAGAGGTTTCTGTGGGAGCACTTC 61
DB 116 GTCCCTGACAGCCCTGCTCATCATGAGAAAGAGGTTTCTGTGGGAGCACTTC 175
QY 62 TGAGCGAGTTCTACATCTTAACGCGAGCCCACTGTCTCT 100
DB 176 TGAGCGAGTTCTACATCTTAACGCGAGCCCACTGTCTCT 214

RESULT 4
R02602 329 bp mRNA linear EST 31-MAR-1995
LOCUS R02602
DEFINITION ye76a02.r1 Soares fetal liver spleen INFIS Homo sapiens cDNA clone

ORGANISM Homo sapiens

REFERENCE	Mammalia; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Xiao,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,Y., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.	
TITLE	Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 98 (20), 15089-15094 (2001)	
MEDLINE	21625106	
COMMENT	Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shouling Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-50801112 Email: hanzg@chgc.sh.cn This clone is available at CHGC in Shanghai.	
FEATURES	Location/Qualifiers	
SOURCE	1..649	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/clone="GK0BE12"	
	/clone_id="GRC"	
	/tissue_type="hepatocellular carcinoma"	
	/dev_stage="Adult"	
	/lab_host="SOLR"	
	/note="Vector: pbluescript sk(-); Site_1: EcoRI; Site_2: XhoI"	
BASE COUNT	142 a	192 c 205 g 110 t
ORIGIN		
Query Match	89.4%; Score 89.4; DB 10; Length 649;	
Best Local Similarity	98.9%; Pred. No. 4,4e-21;	
Matches	90; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	10	CAGGCCCTGCTCATCATGAGGAAACGAGGGTTCTGTGTGTAACCATCTTGAGCGAG 69
Db	6	CAGGCCCTGCTCATCAAGAGGAAACGAGGGTTCTGTGTGTAACCATCTTGAGCGAG 65
OY	70	TTTACATCTTAACGGCGAGCCACAGTCTCT 100
Db	66	TTTACATCTTAACGGCGAGCCACAGTCTCT 96
RESULT 6		
LOCUS	BMS46790	1049 bp mRNA linear EST 20-FEB-2002
DEFINITION	AGENCOURT_6491143 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5723510	
ACCESSION	5, mRNA sequence.	
VERSION	BMS46790	
KEYWORDS	BMS46790.1 GI:18780039	
SOURCE	EST.	
ORGANISM	human.	
	Homo sapiens	
	Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	
REFERENCE	1 (bases 1 to 1049)	
AUTHORS	NIH-MGC http://mhc.nci.nih.gov/.	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: rgabs-remail.nih.gov Tissue Procurement: Invitrogen cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMML) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMML at: http://image.llnl.gov Plate:LLAM12711 row: e column: 15	

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/organism="Homo sapiens"  
/db_xref="GDB:3794720"  
/db_xref="taxon:9606"  
/clone="IMAGE:245474"
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Query Match	81.6%;	Score 81.6;	DB 9;	Length 984;
Best Local Similarity	95.0%;	Pred. No. 3.4e-18;		
Matches 95; Conservative	0;	Mismatches 4;	Indels 1;	Gaps 1;

RESULT	10
AL521984	
LOCUS	
DEFINITION	898 bp mRNA linear EST 13-FEB-2001
ACCESSION	AL521984.LTI.NFL004.NBC2 Homo sapiens CDNA clone CS0DB07YC01.5
VERSION	AL521984
KEYWORDS	GI:12785477
SOURCE	EST.
	human.

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithem@mail.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with `phred`
`v0.98b0904.e`. Vector identified by `cross-match` with the `-mmscore 18`
and `-match 12` options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTTCCAGTCACGAGC
Plate: 97 row: M column: 13
Seq primer: ATTTAGGTGACACTATAG

BASE COUNT	111 a	164 c	182 g	64 t
ORIGIN				

Query Match	70.8%;	Score 70.8;	DB 12;	Length 521;
Best Local Similarity	86.7%;	Pred. No. 1.7e-14;		
Matches 78; Conservative	0;	Mismatches 12;	Indels 0;	Gaps 0;

RESULT	12
W70576	
LOCUS	
DEFINITION	609 bp mRNA linear EST 17-JUN-1996
	me2a04.r1 Soares mouse embryo NM013.5 14.5 Mus musculus cDNA
	clone IMAGE:390126 5' similar to gb:M57285 COAGULATION FACTOR X
	PRECURSOR (HUMAN);, mRNA sequence.

BASE COUNT	157 a	150 c	177 g	125 t
ORIGIN				

Query Match	64.48;	Score 64.4;	DB 14;	Length 609;
Best Local Similarity	78.68;	Pred. No. 3.7e-12;		
Matches 77; Conservative	0;	Mismatches 21;	Indels 0;	Gaps 0;

RESULT 13	
W70579	
LOCUS	W70579 617 bp mRNA linear EST 17-JUN-1996
DEFINITION	me2b03.r1 Soares mouse embryo NDME13.5 14.5 Mus musculus cDNA
	clone IMAGE:390125 5' similar to gb:U57285 COAGULATION FACTOR X
	PRECURSOR (HUMAN); , mRNA sequence.
ACCESION	W70579

FEATURES	Location/Qualifiers
source	1. .609

FEATURES	Location/Qualifiers
source	1. .617

74 ACATCCTAACGGCAGCCCACTGTCTC 99

Thu Jan 16 09:32:18 2003

100396_copy_1_100.rst

Page 8

Db 61 ACAFCCCACTGCTGCCCACTGCTC 86

Search completed: January 15, 2003, 21:18:51
Job time : 1272 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 15, 2003, 17:56:05 ; Search time 1334 Seconds

(without alignments)
2181.620 Million cell updates/sec

Title: 100396_COPY_1_100

Perfect score: 100

Sequence: 1 CGTCTGTACAGAGCCCTGCT.....AACGACAGCCCACTGCTCT 100

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Listing first 45 summaries

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1: gb_da:*
2: gb_hg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_ov:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hg_hum:*
31: em_hg_inv:*
32: em_hg_other:*
33: em_hg_mus:*
34: em_hg_pln:*
35: em_hg_rnd:*
36: em_hg_mem:*
37: em_hg_vrt:*
38: em_sy:*
39: em_hg_hum:*
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41: em_hggo_other:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	100	100.0	142 9 HUMEX7	100396 Human facto
2	100	100.0	132933 9 AL137002	AL137002 Human DNA
3	98.4	98.4	29488 9 AF503510	AF503510 Homo sapi
4	92.6	92.6	725 6 AR121387	AR121387 Sequence
5	92.6	92.6	725 6 AR124119	AR124119 Sequence
6	92.6	92.6	725 6 AX022601	AX022601 Sequence
7	92.6	92.6	725 6 E36142	E36142 ChimERIC se
8	92.6	92.6	1126 6 AR095306	AR095306 Sequence
9	92.6	92.6	1126 6 AR103990	AR103990 Sequence
10	92.6	92.6	1126 9 HUMEX7	AR103990 Human facto
11	92.6	92.6	1404 6 A93124	A93124 Sequence 15
12	92.6	92.6	1414 9 HUMEX7	M2613 Human biolo
13	91	91.0	1443 9 HUMEX7	R03194 Human facto
14	91	91.0	1467 6 A86859	A86859 Sequence 43
15	91	91.0	1467 6 A86886	A86886 Sequence 26
16	91	91.0	1467 6 AX082959	AX082959 Sequence
17	91	91.0	1500 6 AR024194	AR024194 Sequence
18	91	91.0	1507 9 HUMEX7	M57285 Human coagu
19	66.8	66.8	20130 10 AF211347	AF211347 Mus muscu
20	66.8	66.8	299880 2 AC127308	AC127308 Mus muscu
21	64.4	64.4	1486 10 AF087644	AF087644 Mus muscu
22	64.4	64.4	1491 10 MNC0AG01X	AJ222677 Mus muscu
23	63.4	63.4	1537 4 BTCEX1	X0673 Bovine mRNA
24	63.4	63.4	1554 6 A73583	A73583 Sequence 1
25	63.4	63.4	1554 6 AR001423	AR001423 Sequence
26	62.8	62.8	1925 10 BC003877	BC003877 Mus muscu
27	61.8	61.8	1500 4 AF003200	AF003200 Oryctolag
28	55.8	55.8	20947 5 AF519546	AF519546 Danio rer
29	48.8	48.8	1497 10 RNFEXRAT	RNFEXRAT R. norvegicu
30	42.8	42.8	2246 5 CHKVAP	D0844 Gallus gall
31	42.6	42.6	1599 4 AF275654	AF275654 Ornithorh
32	37.4	37.4	164553 2 AC129680	AC129680 Rattus no
33	37.4	37.4	192453 2 AC129457	AC129457 Rattus no
34	37.2	37.2	855 10 GPR1XA	M26237 Guinea pig
35	36	36.0	846 10 RPR1XA	M26247 Rat factor
36	36	36.0	852 10 MUR1XA	M26236 Mouse facto
37	36	36.0	1047 6 AX250084	AX250084 Sequence
38	36	36.0	2697 10 MUR1XA	M23109 Mouse coagu
39	36	36.0	219448 2 AL671984	AL671984 Mus muscu
40	35.2	35.2	111516 5 AL672083	AL672083 Zebrafish
41	34.4	34.4	1360 3 AY118979	AY118979 Drosophill
42	34.4	34.4	95613 2 AC020389	AC020389 Drosophill
43	34.4	34.4	155840 2 AC006495	AC006495 Drosophill
44	34.4	34.4	199044 3 AC009394	AC009394 Drosophill
45	34.4	34.4	224896 3 AE003721	AE003721 Drosophill

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SEGMENT	SOURCE	ORGANISM	REFERENCE
1	HUMEX7	Human factor X (blood coagulation factor) gene, exon 7.	100396	GI.182828	Stuart factor; blood coagulation factor; factor X; glycoprotein; serine protease.	7 of 8	Homo sapiens (tissue library: of Lawn et al., and Yoshitake et al.)	Homo sapiens	1 (bases 1 to 142)
	LOCUS	Human factor X (blood coagulation factor) gene, exon 7.	100396	GI.182828	Stuart factor; blood coagulation factor; factor X; glycoprotein; serine protease.	7 of 8	Homo sapiens (tissue library: of Lawn et al., and Yoshitake et al.)	Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	


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repeat_region /note="2 copies 21 mer 100% conserved"
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1157..13200
repeat_region /note="LIM1 repeat: matches 690..733 of consensus"
13806..14155
repeat_region /note="5 copies 70 mer 82% conserved"
15491..15973
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/evidence=not_experimental
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16278..16371
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16956..17159
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19411..19587
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20202..20342
repeat_region /note="3 copies 47 mer 96% conserved"
20473..20564
repeat_region /note="12 repeat: matches 2602..2693 of consensus"
20816..21894
misc_feature /note="CpG island"
/evidence=not_experimental
repeat_region /note="LIM4 repeat: matches 3584..3686 of consensus"
24570..24680
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24681..24999
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25000..25306
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25311..25620
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25345..25989
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/evidence=not_experimental
repeat_region /note="Alu repeat: matches 1..304 of consensus"
25755..26053
repeat_region /note="Alu repeat: matches 1..304 of consensus"
27585..27688
repeat_region /note="4 copies 26 mer 74% conserved"
27733..27981
repeat_region /note="Alu repeat: matches 9..282 of consensus"
29431..29498
repeat_region /note="MER81 repeat: matches 4..72 of consensus"
29553..29870
repeat_region /note="Alu repeat: matches 1..309 of consensus"
30907..31396
repeat_region /note="7 copies 70 mer 64% conserved"
30908..31432
repeat_region /note="15 copies 35 mer 61% conserved"
30911..31412
repeat_region /note="251 copies 2 mer 99 61% conserved"
30938..31413
repeat_region /note="17 copies 28 mer 61% conserved"
30973..31420
repeat_region /note="14 copies 32 mer 61% conserved"
30987..31385
repeat_region /note="7 copies 57 mer 64% conserved"
31000..31080
misc_feature /note="Sequence from uni-directional dGMP big dye
terminator reads only."
31043..31413
repeat_region /note="7 copies 53 mer 63% conserved"
31078..31415
repeat_region /note="13 copies 26 mer 62% conserved"
31136..31417
repeat_region /note="6 copies 47 mer 66% conserved"
31152..31421
repeat_region /note="9 copies 30 mer 61% conserved"
31153..31267
misc_feature /note="Single clone region. Sequence from reads from a
short insert library derived from a single pUC clone.
Restriction digest data confirm the assembly."
31153..31267

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repeat_region 31175..31426
/note="12 copies 21 mer 61% conserved"
repeat_region 31268..31411
/note="9 copies 16 mer 64% conserved"
misc_feature 31268
/note="Tandem repeat. Forced join. Gap size estimated to
be approximately 350bp by restriction digest data."
repeat_region /note="21 copies 51 mer 89% conserved"
31882..32952
repeat_region /note="62 copies 17 mer 89% conserved"
31884..32937
repeat_region /note="62 copies 17 mer 89% conserved"
31896..35863
misc_feature /note="CpG island"
/evidence=not_experimental
repeat_region 31982..33941
/note="28 copies 70 mer 54% conserved"
32243..32434
repeat_region /note="6 copies 32 mer 64% conserved"
32271..32535
repeat_region /note="5 copies 53 mer 64% conserved"
32883..32952
repeat_region /note="2 copies 35 mer 92% conserved"
33336..33475
repeat_region /note="4 copies 35 mer 70% conserved"
33367..33893

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Query Match 100.0%; Score 100; DB 9; Length 132933;
Best Local Similarity 100.0%; Pred. No. 3.5e-24;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CGTCTGTACAGGCGCTGTCTATCATGAGGAAACAGGAGGTTCTGTGTGAACCAT 60
Db 72010 CGTCTGTACAGGCGCTGTCTATCATGAGGAAACAGGAGGTTCTGTGTGAACCAT 72069
Qy 61 CTGAGCGAGTTCTATCATCTACGCGAGCCCATCTCTCT 100
Db 72070 CTGAGCGAGTTCTATCATCTACGCGAGCCCATCTCTCT 72109

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RESULT 3
AF503510 29488 bp DNA linear PRI 22-MAY-2002
LOCUS Homo sapiens coagulation factor X (F10) gene, complete cds.
DEFINITION AF503510
ACCESSION AF503510.1 GI:20336662
VERSION
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (Bases 1 to 29488)
AUTHORS Ozuna, M., Peel, C.L., Toth, E.J., Yi, Q. and Nickerson, D.A.
TITLE Direct Submission
JOURNAL Submitted (17-APR-2002) Genome Sciences, University of Washington,
1705 NE Pacific, Seattle, WA 98195, USA
COMMENT To cite this work please use: SeattleSNPs, NHLBI H66682 Program
for Genomic Applications, UW-FHCRC, Seattle, WA (URL:
http://pga.gs.washington.edu).
FEATURES
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1..29488
/organism="Homo sapiens"
/db_xref="taxon:9606"
152
/feature="0.04"
/replace="c"
167
/feature="0.01"
/replace="t"
370
/feature="0.01"
/replace="a"
577

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671
variation      /frequency="0.01"
                /replace="t"
713
variation      /frequency="0.12"
                /replace="c"
851
variation      /frequency="0.01"
                /replace="g"
866
variation      /frequency="0.02"
                /replace="a"
880
variation      /frequency="0.05"
                /replace="c"
1116
variation      /frequency="0.79"
                /replace="t"
1169
variation      /frequency="0.02"
                /replace="a"
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                /rpt_type="dispersed"
1319..1324
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1451
variation      /frequency="0.33"
                /replace="a"
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variation      /frequency="0.01"
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1632
variation      /frequency="0.01"
                /replace="t"
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                GKACILPGLPCKQYLERKRSVAQATSSSGAPDSITWKPYDADLDPTENPFDL
                DFNQOTPERGDNMLTRIVGQBCKDECPQALLINEENKFCGGLILSFYILTAH
                CLYQAKRFKRVGDRNTEDEEGEAVHE/EVVKHNRFTKETDFDIAYVRLTPIF
                RMNVAPACILPERDMAESTLMTOKTGIVS:EGRTHEKRGROSTRKMLEVPYVDRNSCKL
                SSSFIITONMFCAGYDTKODACQDSG:PHYTRFKDTYFVTGI:SMGECARNGKKG
                IYKVTAFKMWIDRSMKTRGLPRAKSHA:EVITSSPLK"
                /gene="F10"
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                /replace="t"
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                /replace="g"
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variation      /gene="F10"

variation      /frequency="0.04"
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2527
variation      /gene="F10"
                /frequency="0.12"
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2757
variation      /gene="F10"
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                /note="Region not scanned for variation"
3544..3975
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                /rpt_type="dispersed"
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variation      /gene="F10"
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                /replace="g"
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variation      /gene="F10"
                /frequency="0.01"
                /replace="c"
4100
variation      /gene="F10"
                /frequency="0.01"
                /replace="t"
4544
variation      /gene="F10"
                /frequency="0.19"
                /replace="c"
4567..4967
                /rpt_family="L2"
                /rpt_type="dispersed"
5128
variation      /gene="F10"
                /frequency="0.01"
                /replace="g"
5300
variation      /gene="F10"
                /frequency="0.02"
                /replace="c"
5413
variation      /gene="F10"
                /frequency="0.13"
                /replace="c"
5521
variation      /gene="F10"
                /frequency="0.11"
                /replace="a"
5540..5950
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                /note="Region not scanned for variation"
5997
variation      /gene="F10"
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6098
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                /replace="a"
6110
variation      /gene="F10"
                /frequency="0.01"
                /replace="c"
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variation      /gene="F10"
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variation /replace="c"
6638. 6641
/gene="F10"
/frequency="0.99"
repeat_region /replace="a"
6943. 7395
/rpt_family="ERV1"
repeat_region /rpt_type-dispersed
7396. 7727
/rpt_family="Alu"
variation /rpt_type-dispersed
7437
/gene="F10"
/frequency="0.01"
repeat_region /replace="a"
7728. 8145
/rpt_family="ERV1"
variation /rpt_type-dispersed
7742
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/frequency="0.01"
/replace="t"

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Best Local Similarity 99.0%; Pred. No. 1.2e-23;

Matches 99; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTGTGACAGGCGCCGTCATCATGAGAAAGAGGTTCTGTGTGAACATT 60

DB 26186 CGTGTGACAGGCGCCGTCATCATGAGAAAGAGGTTCTGTGTGAACATT 26245

QY 61 CTGAGCGAGTTCTACATCTTAACGCGAGCCCACTGTCTCT 100

DB 26246 CTGAGCGAGTTCTACATCTTAACGCGAGCCCACTGTCTCT 26285

RESULT 4
ARI21387
LOCUS ARI21387 725 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 12 from patent US 6159722.

ACCESSION ARI21387

VERSION ARI21387.1 GI:14104963

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 725)

AUTHORS Bode,W., Engh,R., Hopfner,K.-P., Huber,R. and Kopetzki,E.

JOURNAL Chimeric serine proteases

PATENT: US 6159722-A 12-12-DEC-2000;

FEATURES

source 1..725

BASE COUNT 172 a 198 c 216 g 139 t

ORIGIN

Query Match 92.6%; Score 92.6; DB 6; Length 725;

Best Local Similarity 96.0%; Pred. No. 1e-21;

Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTCTGTACAGGCGCCGTCATCATGAGAAAGAGGTTCTGTGTGAACATTTC 61

DB 65 GTCCCTGGCAGGCGCCGTCATCATGAGAAAGAGGTTCTGTGTGAACATTTC 124

QY 62 TGAGCGAGTTCTACATCTTAACGCGAGCCCACTGTCTCT 100

DB 125 TGAGCGAGTTCTACATCTTAACGCGAGCCCACTGTCTCT 163

RESULT 5

ARI24119

LOCUS ARI24119 725 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 12 from patent US 6171842.

ACCESSION ARI24119
VERSION ARI24119.1 GI:1109480

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 725)

AUTHORS Bode,W., Engh,R., Hopfner,K.-P., Huber,R. and Kopetzki,E.

JOURNAL Chimeric serine proteases

PATENT: US 6171842-A 12-09-JAN-2001;

FEATURES

source 1..725

BASE COUNT 172 a 198 c 216 g 139 t

ORIGIN

Query Match 92.5%; Score 92.6; DB 6; Length 725;

Best Local Similarity 96.0%; Pred. No. 1e-21;

Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTCTGTACAGGCGCCGTCATCATGAGAAAGAGGTTCTGTGTGAACATTTC 61

DB 65 GTCCCTGGCAGGCGCCGTCATCATGAGAAAGAGGTTCTGTGTGAACATTTC 124

QY 62 TGAGCGAGTTCTACATCTTAACGCGAGCCCACTGTCTCT 100

DB 125 TGAGCGAGTTCTACATCTTAACGCGAGCCCACTGTCTCT 163

RESULT 6

AX022601

LOCUS AX022601 725 bp DNA linear PAT 07-SEP-2000

DEFINITION Sequence 12 from Patent EP0927764.

ACCESSION AX022601

VERSION AX022601.1 GI:10046158

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 725)

AUTHORS Bode,W., Engh,R., Hopfner,K., Kopetzki,E. and Hopfner,K.P.

JOURNAL Chimeric serine proteases

PATENT: EP 0927764-A 12-07-JUL-1999;

FEATURES

source 1..725

BASE COUNT 172 a 198 c 216 g 139 t

ORIGIN

Query Match 92.6%; Score 92.6; DB 6; Length 725;

Best Local Similarity 96.0%; Pred. No. 1e-21;

Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTCTGTACAGGCGCCGTCATCATGAGAAAGAGGTTCTGTGTGAACATTTC 61

DB 65 GTCCCTGGCAGGCGCCGTCATCATGAGAAAGAGGTTCTGTGTGAACATTTC 124

QY 62 TGAGCGAGTTCTACATCTTAACGCGAGCCCACTGTCTCT 100

DB 125 TGAGCGAGTTCTACATCTTAACGCGAGCCCACTGTCTCT 163

RESULT 7

E36142

LOCUS E36142 725 bp DNA linear PAT 18-JUN-2001

DEFINITION Chimeric serine protease.

ACCESSION E36142

VERSION E36142.1 GI:13022520

KEYWORDS JP 1999235173-A/12.

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 725)
 AUTHORS Wolfran, B., Richard, E., Karl, P. H., Robert, H. and Erhard, K.
 TITLE Chimeric serine protease
 JOURNAL Patent: JP 1999235173-A 12 31-AUG-1999;
 ROCHE DIAGNOSTICS GMBH

COMMENT OS Artificial Sequence
 PN JP 1999235173-A/12
 PD 31-AUG-1999
 PE 03-DEC-1998 JP 1998343777
 PR 03-DEC-1997 EP 97121232.9
 PT WOLFRAN BODO, RICHARD ENGEL, KARL PATER HOFNER, ROBERT HYDRA, PI
 ERHARD KOEPEL

PC C12N9/50, C12N1/21, C12N15/09, C12N19/50, C12N1/19, C12N1/21, PC
 C12N1/19, PC
 PC (C12N15/09, C12N1/21, C12N15/00, C12N15/00, C12N1/21) CC

FEATURES
 source 1..725
 Location/Qualifiers
 FT key 1..725
 Location/Qualifiers

BASE COUNT 172 a 198 c 216 g 139 t
 ORIGIN

Query Match 92.6%; Score 92.6; DB 6; Length 725;
 Best Local Similarity 96.0%; Pred. No. 1e-21;
 Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTCTGCACAGCCCTGCTCATCATGAGAAACAGAGGTTCTGTGTGAACCATTC 61
 ||| |
 DB 65 GTCCCTGGCAGGCCCTGCTCATCATGAGAAACAGAGGTTCTGTGTGAACCATTC 124
 ||| |

QY 62 TGAGCGAGTTCTACATCTAACGGCAGCCACTGTCTCT 100
 ||| |
 DB 125 TGAGCGAGTTCTACATCTAACGGCAGCCACTGTCTCT 163
 ||| |

RESULT 8
 LOCUS AR095306 1126 bp DNA linear PAT 08-SEP-2000
 DEFINITION Sequence 27 from patent US 6004555.
 ACCESSION AR095306
 VERSION AR095306.1 GI:10023064
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1126)
 AUTHORS Thorpe, P. E. and Edgington, T. S.
 TITLE Methods for the specific coagulation of vasculature
 JOURNAL Patent: US 6004555-A 27 21-DEC-1999;
 FEATURES Location/Qualifiers
 source 1..1126
 /organism="unknown"

BASE COUNT 269 a 341 c 342 g 174 t
 ORIGIN

Query Match 92.6%; Score 92.6; DB 6; Length 1126;
 Best Local Similarity 96.0%; Pred. No. 1e-21;
 Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTCTGCACAGCCCTGCTCATCATGAGAAACAGAGGTTCTGTGTGAACCATTC 61
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 DB 395 GTCCCTGGCAGGCCCTGCTCATCATGAGAAACAGAGGTTCTGTGTGAACCATTC 454
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QY 62 TGAGCGAGTTCTACATCTAACGGCAGCCACTGTCTCT 100
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 DB 455 TGAGCGAGTTCTACATCTAACGGCAGCCACTGTCTCT 493
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RESULT 9

AR103990
 LOCUS AR103990 1126 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 27 from patent US 6093399.
 ACCESSION AR103990
 VERSION AR103990.1 GI:12816698
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1126)
 AUTHORS Thorpe, P. E. and Edgington, T. S.
 TITLE Methods and compositions for the specific coagulation of
 vasculature
 JOURNAL Patent: US 6093399-A 27 25-JUL-2000;
 FEATURES Location/Qualifiers
 source 1..1126
 /organism="unknown"

BASE COUNT 269 a 341 c 342 g 174 t
 ORIGIN

Query Match 92.6%; Score 92.6; DB 6; Length 1126;
 Best Local Similarity 96.0%; Pred. No. 1e-21;
 Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTCTGCACAGCCCTGCTCATCATGAGAAACAGAGGTTCTGTGTGAACCATTC 61
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 DB 395 GTCCCTGGCAGGCCCTGCTCATCATGAGAAACAGAGGTTCTGTGTGAACCATTC 454
 ||| |

QY 62 TGAGCGAGTTCTACATCTAACGGCAGCCACTGTCTCT 100
 ||| |
 DB 455 TGAGCGAGTTCTACATCTAACGGCAGCCACTGTCTCT 493
 ||| |

RESULT 10
 LOCUS HUMFX 1126 bp mRNA linear PRI 08-NOV-1994
 DEFINITION Human factor X mRNA.
 ACCESSION K01886
 VERSION K01886.1 GI:182820
 KEYWORDS
 SOURCE Human liver, cDNA clone lambda-X-1137.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1126)
 AUTHORS Leytus, S. P., Chung, D. W., Kistiel, W., Kurachi, K. and Davis, E. W.
 TITLE Characterization of a cDNA coding for human factor X
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 81 (12), 3699-3702 (1984)
 MEDLINE 84222026
 PUBMED 6587384

COMMENT In processing, factor X (Stuart factor) is converted to Xa by
 cleavage of a glycoprotein from the amino-terminal end of the heavy
 chain. It then acts as a serine protease in converting prothrombin
 to thrombin.

FEATURES Location/Qualifiers
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 /db_xref="taxon:9606"
 /map="13q34"

gene
 mRNA

CDS

/gene="F10"
 /product="factor X mRNA"
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 /protein_id="AA52486.1"
 /db_xref="GI:182821"
 /db_xref="GDB:G00-119-890"
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 mat_peptide
 mat_peptide

BASE COUNT 269 a 341 c 342 g 174 t
 ORIGIN 5 bp upstream of Tagi site.

Query Match 92.6%; Score 92.6; DB 9; Length 1126;
 Best Local Similarity 96.0%; Pred. No. 1e-21;
 Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

LOCUS A93124 1404 bp DNA linear PAT 22-JAN-2000
 DEFINITION Sequence 15 from Patent WO9747737.
 ACCESSION A93124
 VERSION A93124.1 GI:6741514
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 1404)
 AUTHORS Kopeckl, E. and Hopfner, K.
 TITLE RECOMBINANT BLOOD-COAGULATION PROTEASES
 JOURNAL Patent: WO 9747737-A 15 DEC 1997;
 KOPETZKI ERHARD (DE); BOEHRINGER MANNHEIM GMBH (DE)
 FEATURES
 source 1..1404
 Location/Qualifiers
 /organism="unidentified"
 /db_xref="taxon:32644"
 ORIGIN 356 a 402 c 425 g 221 t

Query Match 92.6%; Score 92.6; DB 6; Length 1404;
 Best Local Similarity 96.0%; Pred. No. 1e-21;
 Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Db 683 GTCCTGACAGGCGCCCTGCTCATCAATGAGAAAACGAGGTTCTGTGGGAACATTC 61
 683 GTCCTGACAGGCGCCCTGCTCATCAATGAGAAAACGAGGTTCTGTGGGAACATTC 742
 QY 62 TGAGCGAGTTCTACATCTTAACGCGACGCCACATGTCCT 100
 743 TGAGCGAGTTCTACATCTTAACGCGACGCCACATGTCCT 781

RESULT 12
 HUMCFX 1414 bp mRNA linear PRI 01-NOV-1994
 LOCUS
 DEFINITION Human blood-coagulation factor X mRNA, complete cds.
 ACCESSION M22613
 VERSION M22613.1 GI:180335
 KEYWORDS
 SOURCE Human liver, cDNA to mRNA, clone PKT218.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1414)
 AUTHORS Kaul, R.K., Hildebrand, B., Roberts, S. and Jagadeeswaran, P.
 TITLE Isolation and characterization of human blood-coagulation factor X
 JOURNAL Gene 41 (2-3), 311-314 (1986)
 MEDLINE 86221713
 PUBMED 3011603
 FEATURES
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 location/Qualifiers
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 /db_xref="taxon:9606"
 /map="13q34"
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 /product="coagulation factor X mRNA"
 <1..1404
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 /note="coagulation factor X precursor"
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 /db_xref="GDB:G00-119-890"
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 /db_xref="GDB:G00-119-890"
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 CELFTRKILSLDNGDCDORCHEONNSVCSPAGYTLAANGACACIPGTYPCGKOTLE
 RRRSVAOATSSSGEAPDSITRPPYAAALDIPENFDLADNTOPEKGNLRTIV
 GGOEKDCRPMOALLINEBNGFCGCTILSEYIITFAHCLYOKRREGDNTLRIV
 GAGVAHEVEVYIKHNFTKETYEDFIALVRLPTIFRANVAPACLPEDMAESTLMT
 OKTIVSGFGRTHKNGROSTRLKMLEVPYDNRNCKLSSTFTITONMFCAGYDTQED
 ACQDSDSGPHVTFKDTYFTVGTIVSWEGCARKKGYITVYAFKLWIDRMTKRL
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sig_peptide
 mat_peptide
 mat_peptide
 mat_peptide

BASE COUNT 358 a 407 c 426 g 223 t

Query Match 92.6%; Score 92.6; DB 9; Length 1414;
 Best Local Similarity 96.0%; Pred. No. 1e-21;
 Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Db 683 GTCCTGACAGGCGCCCTGCTCATCAATGAGAAAACGAGGTTCTGTGGGAACATTC 61
 683 GTCCTGACAGGCGCCCTGCTCATCAATGAGAAAACGAGGTTCTGTGGGAACATTC 742
 QY 62 TGAGCGAGTTCTACATCTTAACGCGACGCCACATGTCCT 100
 743 TGAGCGAGTTCTACATCTTAACGCGACGCCACATGTCCT 781

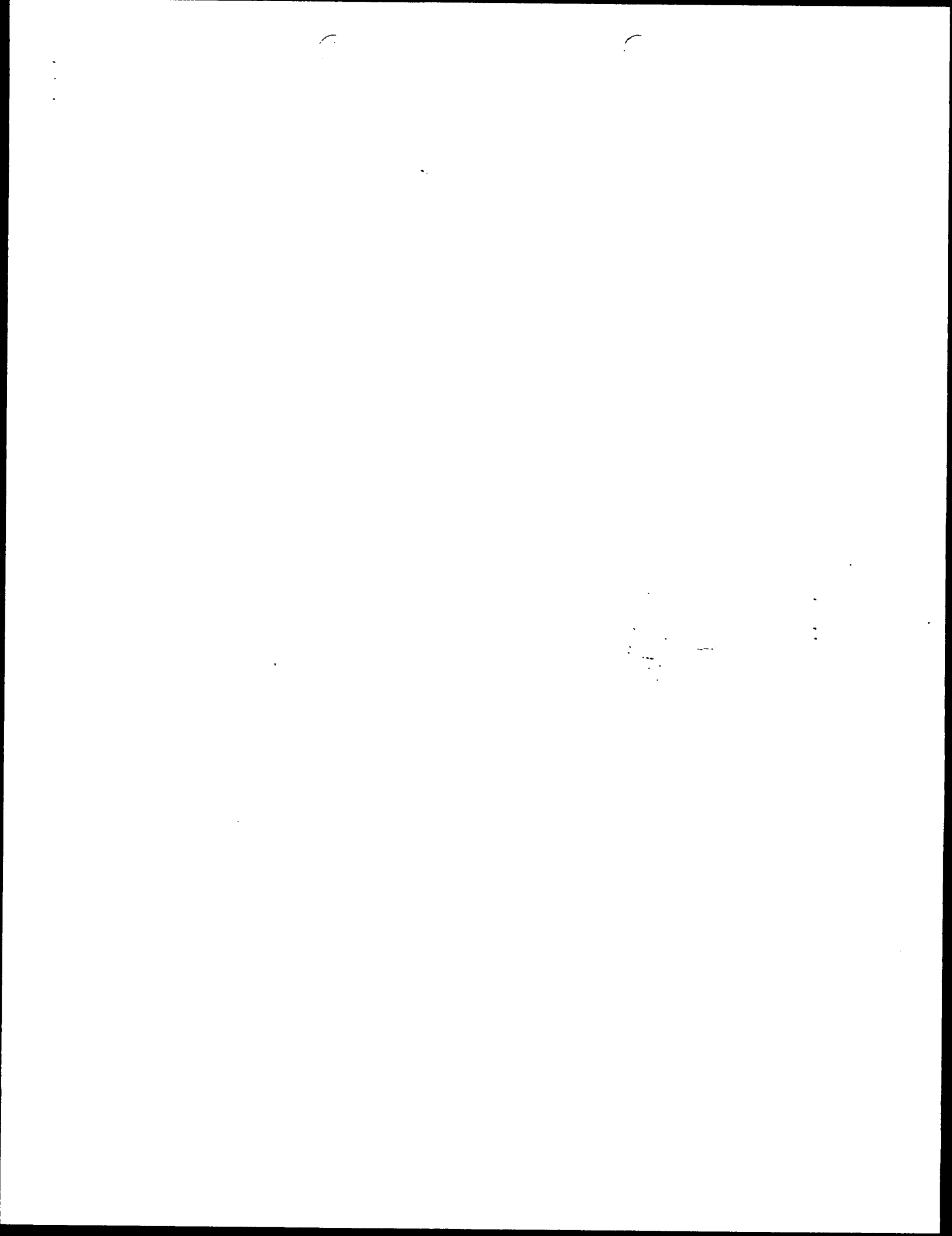
RESULT 13
 HUMCFX 1443 bp mRNA linear PRI 08-NOV-1994
 LOCUS
 DEFINITION Human factor X mRNA, partial signal pept and complete mature pept
 cds.
 ACCESSION K03194
 VERSION K03194.1 GI:182840
 KEYWORDS
 SOURCE Human adult liver, cDNA to mRNA, clones pchX[5,8,14].

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 GKACIPGPYPCGKQTLERKRKSVQAATSSSGEAPDSITWRPYDADLDPTENPDL
 DFNQTOBERGDNMLTRIVGQECCKDECPQOALLINENEGFCGGTILSEFYILTAH
 CLYOAKRFKRVGDRNTEOEGGEAVHEVEVYIKHNFTKRETYDPIAVIRLKTPTF
 RMNVAPACLPERDMAESTLMTOKTGIVSGRPTHEKROSTRILKMLEVFPVDNSCKL
 SSSFIITQNNFCAGYDIKQDADACGDSGGPHVTRFKDTIFVTGIVSMGESCARRGKYG
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BASE COUNT 363 a 424 c 444 g 236 t
 ORIGIN

Query Match 91.0%; Score 91; DB 6; Length 1467;
 Best Local Similarity 94.9%; Pred. No. 3.9e-21;
 Matches 94; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 2 GTCGTGACAGGCCCTGCTCATCAATGAGGAAACGAGGGTTTCTGTGTGGAACCATTC 61
 737 GTCCCTGGCAGGCCCTGCTCATCAATGAGGAAACGAGGGTTTCTGTGTGGAACCATTC 796
 62 TGAGCGAGTCTTATGCTTAACGCGACCCACTGTCTCT 100
 Db 797 TGAGCGAGTCTTATGCTTAACGCGACCCACTGTCTCT 835

Search completed: January 15, 2003, 20:35:36
 Job time : 1354 secs



**ORIGINAL
COPY**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	100	100.0	236	21	AAC70863	Single nucleotide
2	99.6	99.6	236	21	AAC70866	Single nucleotide
3	92.6	92.6	725	20	AAH78022	Chimeric serine pro
4	92.6	92.6	1126	20	AAH15427	DNA encoding coagu
5	92.6	92.6	1126	21	AAAB9786	DNA encoding coagu
6	92.6	92.6	1126	21	AAAI2970	DNA encoding Factor
7	92.6	92.6	1126	21	AAZ51652	Vitamin-K-dependent
8	92.6	92.6	1404	19	AAV10462	Human factor X pro
9	92.6	92.6	1560	22	AAE24733	Nucleotide sequenc

10	92.6	1860	22	AAE244778	Nucleotide sequenc
11	91.6	1467	19	AAV56776	Human Factor X gene
12	91.0	1467	19	AAV56821	Human Factor X gene
13	91.0	1467	22	AAV59409	Human factor X nucle
14	91.0	1507	21	AAV54031	Human factor X codon
15	91.0	1887	22	AAH57469	Human liver cell s
16	75.2	591	24	ABK30368	Human G-protein-co
17	63.4	1554	15	AAW71243	Serine protease fo
18	36	1028	21	AAH61561	CDNA encoding mous
19	34.4	1250	23	ABH12381	Drosophila melanog
20	34.4	3250	23	ABH12390	Drosophila melanog
21	34.4	9594	23	ABH13694	Drosophila melanog
22	34.2	699	18	AAAT79127	Human serine prote
23	34.2	1189	24	AAAT64290	Protease D-g catay
24	34.2	1305	22	AAQ02556	Human seripancrin
25	34.2	1479	22	ADP02557	Human seripancrin
26	34.2	1795	22	AAH26880	Human CDNA encodin
27	34.2	1854	22	AAH99574	Human protein enco
28	34.2	2038	20	AAH87154	Human protease HTP
29	34.2	2063	21	AAH37099	Human PRO1570 (UW)
30	34.2	2063	22	AAH46089	Human DNA encoding
31	34.2	2063	22	AAH92113	Human PRO1570 CDNA
32	34.2	2063	22	AAH54396	DNA encoding prote
33	34.2	2063	24	ABK11090	CDNA encoding tumo
34	34.2	2079	22	AAH13169	Human transmembran
35	34.2	2079	24	AAH72975	CJ48 CDNA. Homo s
36	34.2	2081	24	AAH72976	CJ48 preferred CDN
37	34.2	2121	24	AAH6484	Human serine prote
38	33.8	804	23	ABH28501	Drosophila melanog
39	33.8	864	23	ABH28900	Drosophila melanog
40	32.8	180	21	AAH289010	Cavea sp. Factor I
41	32.6	2137	22	AAH13114	Human membrane-ty
42	32.0	817	23	ABH04003	Drosophila melanog
43	32.0	846	23	ABH17189	Drosophila melanog
44	32	864	19	AAV04616	Flea serine protea
45	32	864	22	AAH08884	Flea serine protea

ALIGNMENTS

RESULT 1	
ID	AAC70863
XX	
XX	AAC70863 standard; DNA; 236 BP.
XX	
AC	AAC70863;
XX	
DT	09-FEB-2001 (first entry)
XX	
DE	Single nucleotide polymorphism containing sequence #231.
XX	
XX	Single nucleotide polymorphism; SNP; human; genetic disease;
KM	disease susceptibility; cardiovascular system; endocrine system
XX	neurological system; forensic testing; paternity testing; ds.
XX	
OS	Homo sapiens.
XX	
PN	MO200058519-A2.
XX	
PD	05-CT-2000.
XX	
PF	30-MAR-2000; 2000MO-0508440.
XX	
PR	31-MAR-1999; 99US-0127248.
XX	
PA	(WHEED) WHITEHEAD INST BIOMEDICAL RES.
PA	(AFFY-) AFFYMETRIX INC.
XX	
PI	Altshuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;
PI	Lipshutz RJ, Patil N, Sklar P;
XX	
DR	WPI; 2000-611722/58.

PT Nucleic acid selected from one of 106 genes comprising single
 PT nucleotide polymorphisms, allele-specific oligonucleotides to the genes
 PT are useful for phenotypic correlations, forensics, paternity testing,
 PT medicine and genetic analysis -
 XX
 PS Claim 1; Fig 5; 214pp; English.

CC The present invention is concerned with a number of human single
 CC nucleotide polymorphisms (SNPs) which the inventors identified in human
 CC genes. These SNPs can be used in disease diagnosis and prediction of an
 CC individual's susceptibility to disease, in forensic and paternity testing
 CC and in genetic mapping. In particular, the SNPs of the invention can be
 CC used to diagnose susceptibility to diseases of the cardiovascular,
 CC endocrine and neurological systems, such as coronary artery disease,
 CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
 CC diseases.

CC Note: The degenerate codon within the sequence represents the position
 CC of an SNP, for example the letter S represents a polymorphism where the
 CC nucleotide may be C or G.

XX Sequence 236 BP; 54 A; 66 C; 67 G; 47 T; 2 other;

Query Match 100.0%; Score 100; LB 21; Length 236;
 Best Local Similarity 100.0%; Pred. No. 1.1e-25;
 Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTGTACAGAGCCCTGCTCATCATGAGGAAAGAGGGTTCTGTGTGGAACCAT 60
 DB 54 CGTCTGTACAGAGCCCTGCTCATCATGAGGAAAGAGGGTTCTGTGTGGAACCAT 113

QY 61 CTGAGCGAGTTCTATCATCTTAACGCGACGCCACCTGTCTCT 100
 DB 114 CTGAGCGAGTTCTATCATCTTAACGCGACGCCACCTGTCTCT 153

RESULT 2
 AAC70866
 ID AAC70866 standard; DNA; 236 BP.

AC AAC70866;
 AC
 DT 09-FEB-2001 (first entry)
 DT
 XX
 XX Single nucleotide polymorphism containing sequence #232.
 DE
 XX Single nucleotide polymorphism; SNP; human; genetic disease;
 KW disease susceptibility; cardiovascular system; endocrine system;
 KW neurological system; forensic testing; paternity testing; ds.
 KW
 XX Homo sapiens.
 XX
 A WO200058519-A2.
 PN
 XX
 PD 05-OCT-2000.
 PD
 XX 30-MAR-2000; 2000WO-US08440.
 PE
 XX 31-MAR-1999; 99US-0127248.
 PR
 XX (WHEED) WHITEHEAD INST BIOMEDICAL RES.
 PA (AFFY-) AFFYMETRIX INC.
 PA
 XX Altschuler D, Gargill M, Daley GO, Ireland JS, Lander ES,
 PI Lipshutz RJ, Patil N, Sklar P;
 PI
 XX WPI; 2000-611722/58.
 DR
 XX Nucleic acid selected from one of 106 genes comprising single
 PT nucleotide polymorphisms, allele-specific oligonucleotides to the genes
 PT are useful for phenotypic correlations, forensics, paternity testing,
 PT medicine and genetic analysis -
 XX
 XX Claim 1; Fig 5; 214pp; English.

XX The present invention is concerned with a number of human single
 CC nucleotide polymorphisms (SNPs) which the inventors identified in human
 CC genes. These SNPs can be used in disease diagnosis and prediction of an
 CC individual's susceptibility to disease, in forensic and paternity testing
 CC and in genetic mapping. In particular, the SNPs of the invention can be
 CC used to diagnose susceptibility to diseases of the cardiovascular,
 CC endocrine and neurological systems, such as coronary artery disease,
 CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
 CC diseases.

CC Note: The degenerate codon within the sequence represents the position
 CC of an SNP, for example the letter S represents a polymorphism where the
 CC nucleotide may be C or G.

XX Sequence 236 BP; 54 A; 66 C; 67 G; 47 T; 2 other;

Query Match 99.6%; Score 99.6; DB 21; Length 236;
 Best Local Similarity 99.0%; Pred. No. 1.6e-25;
 Matches 99; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTGTACAGAGCCCTGCTCATCATGAGGAAAGAGGGTTCTGTGTGGAACCAT 60
 DB 54 CGTCTGTACAGAGCCCTGCTCATCATGAGGAAAGAGGGTTCTGTGTGGAACCAT 113

QY 61 CTGAGCGAGTTCTATCATCTTAACGCGACGCCACCTGTCTCT 100
 DB 114 CTGAGCGAGTTCTATCATCTTAACGCGACGCCACCTGTCTCT 153

RESULT 3
 AAX78022
 ID AAX78022 standard; DNA; 725 BP.

AC AAX78022;
 AC
 DT 19-AUG-1999 (first entry)
 DT
 XX
 XX Chimeric serine protease FXT DNA.
 DE
 XX Serine protease; chim rlc; antithrombotic; modulator; drug design;
 KW 3-D crystal structure; crystallization; hematopoietic cascade;
 KW FXT; ss.
 KW
 XX Synthetic.
 OS
 XX EP927764-A2.
 PN
 XX 07-JUL-1999.
 PD
 XX 27-NOV-1998; 98EP-0122481.
 PE
 XX 03-DEC-1997; 97EP-0121232.
 PR
 XX (HOFF) ROCHE DIAGNOSTICS GMBH.
 PA
 XX Bode W, Engh R, Hopfner K, Huber R, Kopetzki E;
 PI
 XX WPI; 1999-359878/31.
 DR
 XX P-PSDB; AAY08894.
 PA
 XX Chimeric serine protease comprising Factor X and Trypsin catalytic
 PT domains, useful for identifying thrombolytic agents
 PT
 XX Example 2; Fig 2; 23pp; German.

CC This invention describes a novel chimeric serine protease compound which
 CC has antithrombotic activity and comprises two domains with a beta-sheet
 CC structure. The first domain corresponds to the first domain of a first
 CC serine protease and the second domain corresponds to the second domain
 CC of a second serine protease. The products of the invention can be used
 CC for identifying antithrombotic agents by determining whether an agent
 CC modulates the activity of the serine protease. They can also be used to
 CC identify agents through rational drug design using information based on

CC its 3-D crystal structure. The chimeric serine protease, is very good
 CC for crystallization and for determining structural data and is also
 CC useful for the identification of specific antithrombotic agents that
 CC unlike prior art agents are extremely specific for only one factor in a
 CC haemopoietic cascade.

SO Sequence 725 BP; 172 A; 198 C; 216 G; 139 T; 0 other;

Query Match 92.6%; Score 92.6; DB 20; Length 725;
 Best Local Similarity 96.0%; Pred. No. 6.6e-23;
 Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GTCGTGCACAGCCCTGCTCATCATGAGAAAGAGGTTCTGTGTGAACCATTC 61

DB 65 GTCCCTGGCAGCCCTGCTCATCATGAGAAAGAGGTTCTGTGTGAACCATTC 124

OY 62 TGAGCGAGTTCTACATCCTTAACGCGAGCCCACTGTCTCT 100

DB 125 TGAGCGAGTTCTACATCCTTAACGCGAGCCCACTGTCTCT 163

RESULT 4
 AAX15427

ID AAX15427 standard; DNA; 1126 BP.

AC AAX15427;

DT 05-MAY-1999 (first entry)

DE DNA encoding coagulation factor X/Xa.

XX Truncated tissue factor; tissue factor binding ligand; coagulation;
 XX disease-associated vasculature; tumour; benign prostatic hyperplasia;
 XX AVV; meningioma; hemangioma; neovascular glaucoma; psoriasis; synovitis;
 XX dematiolitis; endometriosis; angiodibroma; rheumatoid arthritis;
 XX atherosclerotic plaque; corneal graft neovascularisation;
 XX haemophilic joint; hypertrophic scar; Osler-Weber syndrome;
 XX pyogenic granuloma; retrolental fibroplasia; scleroderma; trachoma;
 XX vascular adhesion; coagulation factor; factor X/Xa; ss.

OS Homo sapiens.

XX US5877289-A.

PD 02-MAR-1999.

PF 07-JUN-1995; 95US-0479733.

XX 07-JUN-1995; 95US-0479733.

PR 05-MAR-1992; 92US-0846349.

PR 02-MAR-1994; 94US-0205330.

PR 11-JUL-1994; 94US-0273567.

PA (SCRI) SCRIpps RES INST.

PI (TEXA) UNIV TEXAS SYSTEM.

PI Edgington TS, Thorpe PE;

PI MPI: 1999-189722/16.

XX Tissue factor binding ligands - comprising first binding region

XX which binds to vasculature, particularly of tumours, and tissue

XX factor construct

XX Example 9; Columns 129-132; 83pp; English.

CC The present sequence encodes a coagulation factor. The specification

CC describes tissue factor binding ligands which comprise a binding region

CC which binds to vasculature, particularly of tumours, and a tissue factor

CC construct. The binding ligands can be used for stimulating coagulation in

CC disease-associated vasculature, particularly for the treatment of

CC tumours. The products can also be used for treating e.g. benign prostatic

CC hyperplasia, diabetic-retinopathy, vascular stenosis, arteriovenous
 CC malformations (AVM), meningioma, hemangioma, neovascular glaucoma,
 CC psoriasis, synovitis, dermatitis, endometriosis, angiodibroma, rheumatoid
 CC arthritis, atherosclerotic plaques, corneal graft neovascularisation,
 CC haemophilic joints, hypertrophic scars, Osler-Weber syndrome, pyogenic
 CC granuloma retrolental fibroplasia, scleroderma, trachoma, or vascular
 CC adhesions. The products can also be used in binding assays.

SO Sequence 1126 BP; 269 A; 341 C; 342 G; 174 T; 0 other;

Query Match 92.6%; Score 92.6; DB 20; Length 1126;
 Best Local Similarity 96.0%; Pred. No. 7.5e-23;
 Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GTCGTGCACAGCCCTGCTCATCATGAGAAAGAGGTTCTGTGTGAACCATTC 61

DB 395 GTCCCTGGCAGCCCTGCTCATCATGAGAAAGAGGTTCTGTGTGAACCATTC 454

OY 62 TGAGCGAGTTCTACATCCTTAACGCGAGCCCACTGTCTCT 100

DB 455 TGAGCGAGTTCTACATCCTTAACGCGAGCCCACTGTCTCT 493

RESULT 5

ID AAA89786

AC AAA89786;

DT 14-DEC-2000 (first entry)

DE DNA encoding coagulation factor X/Xa.

XX Tissue factor protein; truncated tissue factor; tTF; cytostatic;
 XX coagulant; diabetic retinopathy; arteriovenous malformation;
 XX meningioma; hemangioma; neovascular glaucoma; psoriasis; synovitis;
 XX endometriosis; hemophilic joint; hypertrophic scar; vascular adhesion;
 XX tumour; cancer; ligand; human; factor X; ds.

OS Homo sapiens.

XX US6093399-A.

PD 25-JUL-2000.

PF 07-JUN-1995; 95US-0482369.

XX 07-JUN-1995; 95US-0482369.

PR 05-MAR-1992; 92US-0846349.

PR 02-MAR-1994; 94US-0205330.

PR 11-JUL-1994; 94US-0273567.

PA (SCRI) SCRIpps RES INST.

PI (TEXA) UNIV TEXAS SYSTEM.

PI Edgington TS, Thorpe PE;

PI MPI: 2000-531471/48.

XX New immunological and growth factor-based bispecific binding ligands,

XX useful for stimulating coagulation in vasculature-associated diseases,

XX e.g. for treating both benign and malignant diseases (e.g. meningioma

XX or hemangioma)

XX Example 9; Column 129-130; 83pp; English.

CC The present invention relates to a binding ligand with a first binding

CC region that is operatively linked to either a coagulation factor or a

CC second binding region that binds to a coagulation factor. The first

CC binding region binds to a component on the surface of a tumour. The

CC second binding region is all or part of an antibody. An example of a

CC coagulation factor for use in the invention is human truncated tissue

CC factor. Truncated tissue factor (tTF) is the extracellular domain of the

CC mature tissue factor protein (see AAB15019). The binding ligand of the

CC invention is useful for stimulating coagulation in vasculature
 CC associated diseases. Particularly, the binding ligand is useful for
 CC treating both benign and malignant diseases that have a vascular
 CC component. These diseases include benign growths (e.g. BPH), diabetic
 CC retinopathy, arteriovenous malformations, meningioma, hemangioma,
 CC neovascular glaucoma, psoriasis, synovitis, endometriosis, hemophylia
 CC joints, hypertrophic scars or vascular adhesions. The present binding
 CC ligands offer the advantage that even limited damage to the tumour
 CC each capillary provides an avalanche of tumour cell death because
 CC cells. The present sequence is DNA encoding coagulation factor
 CC X/Xa. This factor was used in the invention.

SO Sequence 1126 BP; 269 A; 341 C; 342 G; 174 T; 0 other;

Query Match 92.6%; Score 92.6; DB 21; Length 1126;
 Best Local Similarity 96.0%; Pred. No. 7.5e-23;
 Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GTCGTGACAGGCCCTGCTCATCATGAGAAACGAGGTTCTGTGTGAACCATTC 61
 395 GTCCTGTGAGGCGCTGCTCATCATGAGAAACGAGTTCTGTGTGAACCATTC 454
 OY 62 TGAGCGAGTTCTACATCTTAACGCGAGCCCACTGTCTCT 100
 455 TGAGCGAGTTCTACATCTTAACGCGAGCCCACTGTCTCT 493

RESULT 6

AA12970
 ID AA12970 standard; DNA; 1126 BP.

AC AAA12970;

DF 18-JUL-2000 (first entry)

DE DNA encoding Factor X/Xa, SEQ ID NO:27.

KW Truncated tissue factor; tTF; human; blood coagulation;

KW tumour vasculature; bispecific antibody; targeting; cancer;

KW vascularised tumour; PCR primer; ss.

OS Homo sapiens.

PN US6036955-A.

PD 14-MAR-2000.

PF 07-JUN-1995; 95US-0479727.

PR 05-MAR-1992; 92US-0846349.

PR 02-MAR-1994; 94US-0205330.

PR 11-JUL-1994; 94US-0273567.

PA (TEXA) UNIV TEXAS SYSTEM.

PA (SCTR) SCRIPPS RES INST.

XX Edgington TS, Thorpe PE;

XX WPI; 2000-269871/23.

XX Kit for inducing coagulation in tumor vasculature, useful for treating

XX malignant or benign growths, contains ligand, linked to coagulation

XX agent, that targets tumor marker

XX Example 9; Columns 131-132; 86pp; English.

XX The invention relates to the induction of blood coagulation specifically

XX within tumour vasculature. This is achieved by the use of a bispecific

XX molecule, which comprises a region capable of binding to intratumoral

XX vascular or stromal cells linked to a coagulation factor or to a region

XX capable of binding to a coagulation factor. An example of such a

XX bispecific molecule is a bispecific antibody, where one arm binds a

CC tumour antigen, and the other arm binds a coagulation factor. The
 CC expression of certain proteins (tumour antigens) is upregulated in
 CC tumour vasculature; such proteins include vascular endothelial growth
 CC factor (VEGF) and members of the fibroblast growth factor (FGF) family.
 CC An antibody or antibody fragment against VEGF or basic FGF (bFGF) may be
 CC incorporated into the bispecific molecule in order to target coagulation
 CC to tumour vasculature. The coagulation factor-binding portion of the
 CC bispecific molecule may be, for example, directed to tissue factor (TF).
 CC A preferred form of TF used in the invention is a truncated form (tTF,
 CC AA18148) which lacks the cytoplasmic and transmembrane domains.
 CC Although tTF can associate with Factor VIIa, the tTF/Factor VIIa complex
 CC cannot alone initiate the coagulation cascade as the complex has to be
 CC associated with a phospholipid surface for coagulation to occur.
 CC However, binding of tTF to tumour vasculature via a tumour antigen/tTF
 CC membrane to enable the initiation of coagulation. Kits for the induction
 CC of tumour vasculature-specific coagulation may be used to treat malignant
 CC or benign diseases associated with a vascular component, particularly
 CC cancers, but also benign growths, prostatic hypertrophy, restenosis,
 CC psoriasis, glaucoma, rheumatoid arthritis. Coagulation is induced
 CC selectively in the tumour vasculature, minimising side effects. Such kits
 CC are likely to be effective against many different types of cancer.
 CC Sequences AA12945-AA12952, AA12954-AA12963 and AA12971-AA12972
 CC represent PCR primers used in exemplifications of the present invention
 CC to generate constructs encoding tTF, tTF variants or tTF dimers.

SO Sequence 1126 BP; 269 A; 341 C; 342 G; 174 T; 0 other;

Query Match 92.6%; Score 92.6; DB 21; Length 1126;
 Best Local Similarity 96.0%; Pred. No. 7.5e-23;
 Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GTCGTGACAGGCCCTGCTCATCATGAGAAACGAGGTTCTGTGTGAACCATTC 61
 395 GTCCTGTGAGGCGCTGCTCATCATGAGAAACGAGGTTCTGTGTGAACCATTC 454
 OY 62 TGAGCGAGTTCTACATCTTAACGCGAGCCCACTGTCTCT 100
 455 TGAGCGAGTTCTACATCTTAACGCGAGCCCACTGTCTCT 493

RESULT 7

AA256120
 ID AA256120 standard; DNA; 1126 BP.

AC AA256120;

DF 27-MAR-2000 (first entry)

DE Vitamin-K-dependent coagulation factor X/Xa coding sequence.

KW Vitamin-K dependent coagulation factor; tumour associated vasculature;

KW carcinoma; benign prostatic hyperplasia; diabetic retinopathy;

KW vascular restenosis; arteriovenous malformation; meningioma; haemangioma;

KW neovascular glaucoma; psoriasis; cytoskeletal; antidiabetic; vasotropic;

KW ophthalmological; antipsoriatic; Factor X/Xa; ss.

OS Unspecified.

PN US6004555-A.

PD 21-DEC-1999.

PF 07-JUN-1995; 95US-0487427.

PR 05-MAR-1992; 92US-0846349.

PR 02-MAR-1994; 94US-0205330.

PR 11-JUL-1994; 94US-0273567.

PA (SCTR) SCRIPPS RES INST.

PA (TEXA) UNIV TEXAS SYSTEM.

XX Edgington TS, Thorpe PE;

XX WPI; 2000-072047/06.

XX Bispecific binding ligands for promoting blood coagulation in a tumour
XX associated vasculature are useful for treating cancer.

XX Example 9: Column 131-132; 83pp; English.

XX This is the coding sequence for Factor X/Xa, a vitamin-K-dependent
XX coagulation factor. This coagulation factor can be used in the formation
XX of coagulants. Mutated versions of this sequence can be used in the
XX method for delivering a coagulant to a tumour-associated vasculature
XX using bispecific binding ligands which promote blood coagulation. The
XX binding ligand consists of a binding region that binds to a
XX surface-expressed, surface accessible or surface-localised component of a
XX tumour cell, intratumoural vasculature or tumour associated stroma. The
XX binding region is linked to a coagulating agent which is a coagulation
XX factor (e.g. tissue factor). The second binding region comprises an
XX antibody or an antigen binding region of an antibody. The method is used
XX for delivering an exogenous or an endogenous coagulation factor to
XX tumour-associated vasculature which is benign or malignant. The method
XX can be used to treat cancer by promoting specific blood coagulation in
XX the vasculature of the tumour relative to the vasculature in nontumour
XX sites. Vascularised tumours are usually solid tumours, particularly
XX carcinomas which require a vascular component to provide oxygen and
XX nutrients. The ligands are suitable to treat benign and malignant
XX hyperplasia, diabetic retinopathy, vascular restenosis, arteriovenous
XX malformations, meningioma, haemangioma, neurovascular glaucoma and
XX portomas. The ligands can also be used in standard binding assays in
XX vitro. Bispecific ligands can also be designed which are capable of binding to
XX vascular endothelial cells and disease-associated agents are similar in
XX different diseases and in different tumours, making it possible to treat
XX numerous diseases and different types of cancer with one pharmaceutical,
XX therefore an agent does not need to be tailored to each individual
XX disease or specific tumour type.

SO Sequence 1126 BP; 269 A; 341 C; 342 G; 174 T; 0 other;

Query Match 92.6%; Score 92.6; DB 21; Length 1126;

Best Local Similarity 96.0%; Pred. No. 7.5e-23;

Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTCTGTACAGGCGCTCTCATATGAGGAGGAGGTTCTGTGTGAGCAATTC 61
DB 395 GTCTGTACAGGCGCTCTCATATGAGGAGGAGGTTCTGTGTGAGCAATTC 454
Y 62 TGAGCGAGTTCTACATCTTAACGCGAGCCACTGTCTCT 100
DB 455 TGAGCGAGTTCTACATCTTAACGCGAGCCACTGTCTCT 493

RESULT 8
AAV10462
ID AAV10462 standard; DNA; 1404 BP.

XX AAV10462;

DT 16-JUN-1998 (first entry)

DE Human Factor X protease cDNA.

XX Factor X; factor IX; serine protease activity; catalytic domain; ZAD;
XX zymogen-activating domain; epidermal growth factor-like domain; EGFL;
XX BGF2; regulator; coagulation; fibrinolysis; homeostasis; X-ray structure;
XX detection; drug modelling; restriction protease; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH 1.1404
FT CDS /tag= a

FT /Product- Factor X
FT /Note- "partial coding sequence"

XX MO9747737-AL.

XX 18-DEC-1997.

XX 11-JUN-1997; 97MO-EP03027.

XX 06-JUL-1996; 96EP-0110959.

XX 11-JUN-1996; 96EP-0109288.

XX 22-JUN-1996; 96EP-0110109.

XX (BOEF) BOEHRINGER MANNHEIM GMBH.

XX Hopfner K, Kopetzki E;

XX WPI; 1998-052304/05.

XX P-PSDB; AAM40283.

XX Non-glycosylated, truncated forms of factor IX family protein with
XX serine protease activity - used to screen for specific modulators
XX and to assay factor IXa

XX Disclosure; Fig 3; 49pp; German.

XX This sequence encodes a human factor X protease. This protein is used
XX in the construction of a novel non-glycosylated protein and truncated
XX and zymogen forms of this protein, which have serine protease activity.
XX The protein is composed of various domains from a factor IX family
XX protein, namely a catalytic domain (CD), N-terminally bound to a
XX zymogen-activating domain (ZAD), N-terminally bound to an EGFL and/or
XX EGFL domain (EGF epidermal growth factor-like domain). Such proteins
XX are used to identify activators/inhibitors of factor IX family proteins
XX (potentially useful as regulators of coagulation, fibrinolysis and
XX homeostasis). The protein in zymogen form is also useful in assays for
XX detecting factor IXa activity in aqueous solution (specifically in body
XX fluids). The protein can be used to produce co-crystals with protease
XX variants or inhibitors for X-ray structural analysis and drug modelling
XX and as restriction proteases in biotechnology. These truncated proteins
XX have the same specificity as factor IX family proteases and can be
XX produced in prokaryotes in a form that allows production of active enzyme
XX by conversion to native form and enzymatic cleavage.

SO Sequence 1404 BP; 356 A; 404 C; 423 G; 221 T; 0 other;

Query Match 92.6%; Score 92.6; DB 19; Length 1404;

Best Local Similarity 96.0%; Pred. No. 8.1e-23;

Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTCTGTACAGGCGCTCTCATATGAGGAGGAGGTTCTGTGTGAGCAATTC 61
DB 683 GTCTGTACAGGCGCTCTCATATGAGGAGGAGGTTCTGTGTGAGCAATTC 742
QY 62 TGAGCGAGTTCTACATCTTAACGCGAGCCACTGTCTCT 100
DB 743 TGAGCGAGTTCTACATCTTAACGCGAGCCACTGTCTCT 781

RESULT 9
AAE24735
ID AAE24735 standard; DNA; 1560 BP.

XX AAE24735;

DT 20-APR-2001 (first entry)

DE Nucleotide sequence of Sig/CBD cex/ER retaining peptide fusion.

XX Protein production; food processing; protein antibiotic; feed enzyme;
XX protein L; CBD cex protein; cell signal peptide; ss.

XX Synthetic.

DT 27-NOV-1998 (first entry)
 XX Human Factor X genomic DNA.
 DE
 XX Factor X; analogue; activation cleavage site; protease; bleeding; human;
 KM Factor IX; Factor VII; Factor VIII; haemophilia; gene therapy; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1467
 FT /*tag= a
 FT /product= "Factor X"
 FT sig_peptide 1..120
 FT /*tag= b
 FT mat_peptide 121..1464
 FT /*tag= c
 FT
 PN WO9838317-A1.
 X 03-SEP-1998.
 /D
 XX
 PF 27-FEB-1998; 98WO-AT00045.
 XX
 PR 27-FEB-1997; 97AT-0000335.
 XX
 PA (IMMO) IMMUNO AG.
 XX
 PI Dörner F, Eibl J, Fisch A, Himmelspach M, Schlokot U;
 XX
 DR WPI; 1998-48121/41.
 DR P-PSDB; AAM76216.
 XX
 PT New factor X analogues with processing site for protease not active
 PT on natural protein - and related DNA, is very stable and can be
 PT activated in vitro or in vivo without using animal protease(s),
 PT particularly for treating disorders of blood coagulation
 PT
 PS Claim 3; Fig 1; 86pp; German.
 XX
 CC This sequence encodes the human Factor X protein which is used in a
 CC method resulting in the production of novel human Factor X (F10)
 CC analogues. Such analogues have in the region of the natural F10a
 CC activation cleavage site, a modification that creates a processing site
 CC for a protease that does not naturally cleave F10 in this region. The
 CC proteins are used to generate, in vivo or in vitro, F10a analogues that
 CC can be used to control bleeding and for treating defects of factors IX,
 CC VII or VIII, e.g. in haemophiliacs who have developed antibodies to
 CC factors VIII and/or IX. The encoding nucleic acid can be used in gene
 CC therapy of the same conditions. The analogues have high stability and can
 CC be activated without use of animal enzymes such as trypsin. Only
 CC activation is affected, their activity is the same as the natural factor.
 CC The analogues can be isolated as a pure single-chain pro-protein (not
 CC usually possible because of rapid processing of the native precursor) and
 CC this converted to two-chain form by subsequent activation. Activated
 CC analogues have good stability and structural integrity and are
 CC practically free of inactive intermediates and autoprolytic
 CC decomposition products.
 CC
 SQ Sequence 1467 BP; 363 A; 424 C; 444 G; 236 T; 0 other;
 Query Match 91.0%; Score 91; DB 19; Length 1467;
 Best Local Similarity 94.9%; Pred. No. 3e-22;
 Matches 94; Conservative 0; Mismatches 5; Indels 0; gaps 0;
 OY 2 GTCGTACAGAGCCCTCTCATCAGAGAAAGAGAGGTTCTGTGTGAAACATTC 61
 DB 737 GTCCCTGCGAGCCCTCTCATCAGAGAAAGAGAGGTTCTGTGTGAAACATTC 796
 OY 62 TGAGCGAGTTCTACATCCTAAGCGAGCCAGCATCTCT 100
 DB 797 TGAGCGAGTTCTACATCCTAAGCGAGCCAGCATCTCT 835

RESULT 12
 ID AAV56821
 XX AAV56821 standard; DNA; 1467 BP.
 AC AAV56821;
 XX
 DT 27-NOV-1998 (first entry)
 XX
 XX Human Factor X genomic DNA.
 DE
 XX Factor X; analogue; activation cleavage site; protease; bleeding; human;
 KM Factor IX; Factor VII; Factor VIII; haemophilia; gene therapy; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1467
 FT /*tag= a
 FT /product= "Factor X"
 FT sig_peptide 1..120
 FT /*tag= b
 FT mat_peptide 121..1464
 FT /*tag= c
 FT
 PN WO9838318-A1.
 X 03-SEP-1998.
 /D
 XX
 PF 27-FEB-1998; 98WO-AT00046.
 XX
 PR 27-FEB-1997; 97AT-0000336.
 XX
 PA (IMMO) IMMUNO AG.
 XX
 PI Dörner F, Eibl J, Falkner F, Himmelspach M, Pfeleiderer M;
 XX
 DR WPI; 1998-48212/41.
 DR P-PSDB; AAM76218.
 XX
 PT New factor 10 deletion mutants lacking the natural protease
 PT processing site - but having a non-natural site inserted, and
 PT related DNA, particularly for in vitro activation to products used
 PT to treat blood coagulation disorders
 PT
 PS Claim 3; Fig 1; 82pp; German.
 XX
 CC This sequence encodes the human Factor X protein which is used in a
 CC method resulting in the production of novel human Factor X (F10)
 CC analogues. Such analogues have in the region of the natural F10a
 CC activation cleavage site, a modification that creates a processing site
 CC for a protease that does not naturally cleave F10 in this region. The
 CC proteins are used to generate, in vivo or in vitro, F10a analogues that
 CC can be used to control bleeding and for treating defects of factors IX,
 CC VII or VIII, e.g. in haemophiliacs who have developed antibodies to
 CC factors VIII and/or IX. The encoding nucleic acid can be used in gene
 CC therapy of the same conditions. The analogues have high stability and can
 CC be activated without use of animal enzymes such as trypsin. Only
 CC activation is affected, their activity is the same as the natural factor.
 CC The analogues can be isolated as a pure single-chain pro-protein (not
 CC usually possible because of rapid processing of the native precursor) and
 CC this converted to two-chain form by subsequent activation. Activated
 CC analogues have good stability and structural integrity and are
 CC practically free of inactive intermediates and autoprolytic
 CC decomposition products.
 CC
 SQ Sequence 1467 BP; 363 A; 424 C; 444 G; 236 T; 0 other;
 Query Match 91.0%; Score 91; DB 19; Length 1467;
 Best Local Similarity 94.9%; Pred. No. 3e-22;
 Matches 94; Conservative 0; Mismatches 5; Indels 0; gaps 0;

QY 2 GTCGTACAGAGCCCTGCTCATATGAGAAAAAGAGGTTTCTGTGTGGAACCATTC 61
DB 737 GTCCCTGGAGCCCTGCTCATATGAGAAAAAGAGGTTTCTGTGTGGAACCATTC 796
QY 62 TGAGCGAGTTCTACATCTTAAGGAGCCGACCTGTCTCT 100
DB 797 TGAGCGAGTTCTACATCTTAAGGAGCCGACCTGTCTCT 835

RESULT 13

AAFS9409

ID AAF59409 standard; cDNA; 1467 BP.

AC AAF59409;

DT 02-MAY-2001 (first entry)

DE Human factor X nucleotide sequence SEQ ID NO:1.

KW Human; factor X; mutant; haemostatic; gene therapy; haemophilia;
blood coagulation disorder; haemophilia; ss.

XN Homo sapiens.

XN WO200110896-A2.

XN 15-FEB-2001.

XN 07-AUG-2000; 2000MO-EP07631.

XN 10-AUG-1999; 99AT-0001377.

XN (BAXT) BAXTER AG.

XN Himmelsbach M, Schlokot U;

XN WPI; 2001-191516/19.

XN P-PSDB; AAB70411.

XN Novel factor X analog useful for producing drug which is useful for
treatment of blood coagulation disorders, such as hemophilia, contains
modification between amino acids Glu226 and Ile235

XN Disclosure; Fig 1; 50pp; English.

The present invention describes a factor X analogue (I) which contains
a modification between Glu226 and Ile235, relative to the 488 residue
amino acid sequence given in AAB70411. (I) has haemostatic activity and
can be used in gene therapy. (I) encoding polynucleotide (II) can be
used to produce a drug, which is useful for treatment of patients with
blood coagulation disorders, such as patients suffering from haemophilia,
or haemophilias with inhibitory antibodies. Preparations containing a
polypeptide with factor X/Xa activity are more readily activated by
factor Xla or its derivative, which has high stability, without having
to use one of the proteases used in prior art to activate the natural
factor X, particularly one of animal origins, such as Russell's viper
venom (RVV) or trypsin. The present sequence encodes human factor X,
which is given in the exemplification of the present invention.

Sequence 1467 BP; 363 A; 424 C; 444 G; 236 T; 0 other;

Query Match 91.0%; Score 91; DB 22; Length 1467;

Best Local Similarity 94.9%; Pred. No. 3e-22;

Matches 94; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GTCGTACAGAGCCCTGCTCATATGAGAAAAAGAGGTTTCTGTGTGGAACCATTC 61

DB 737 GTCCCTGGAGCCCTGCTCATATGAGAAAAAGAGGTTTCTGTGTGGAACCATTC 796

QY 62 TGAGCGAGTTCTACATCTTAAGGAGCCGACCTGTCTCT 100

DB 797 TGAGCGAGTTCTACATCTTAAGGAGCCGACCTGTCTCT 835

RESULT 14

ID AAA54031

AAA54031 standard; DNA; 1507 BP.

AC AAA54031;

DT 08-FEB-2001 (first entry)

DE Human factor X coding sequence.

KW Vitamin K dependent protein; VKDP; gamma-carboxylation; chimeric
protein; fusion protein; coagulation factor; Factor X; Factor VII;
protein S; Factor IX; Protein C; prothrombin; blood clotting;
haemophilia; human; de

XN Homo sapiens.

XN WO200054787-A1.

XN 21-SEP-2000.

XN 16-MAR-2000; 2000MO-US06934.

XN 16-MAR-1999; 99US-0124609.

XN (CHIL-) CHILDRENS HOSPITAL, PHILADELPHIA.

XN (UYNC-) UNIV NORTH CAROLINA.

XN High KA, Camire RM, Larson PJ, Stafford DW;

XN WPI; 2000-638152/61.

Chimeric DNA for optimizing gamma carboxylation of vitamin K-dependent
protein useful for treating diseases associated with the protein,
protein S; Factor IX; Protein C; prothrombin; blood clotting;
haemophilia; human; de

XN Disclosure; Fig 6a; 60pp; English.

Efficient processing and release of mature two-chain factor X into
the circulation requires: removal of the signal sequence; formation
of disulfide bonds; modification of amino terminal glutamic acid
residues, to gamma-carboxyglutamic acid; modification of one
aspartic acid in the first epidermal growth factor (EGF) domain to
beta-hydroxyaspartic acid; addition of N- and O-linked
oligosaccharides to the activation peptide; removal of an internal
tripeptide to yield two-chain factor X and removal of the
propeptide just prior to secretion. While some of these modifications
do not appear essential for factor X function the removal of the
signal sequence, propeptide, internal tripeptide and full
gamma-carboxylation are all steps which are important requisites for
the production of biologically active factor X/FXa. Isolated chimeric
polynucleotides are described which encode a propeptide fused to a
nucleic acid sequence encoding a vitamin K-dependent protein (VKDP).
The fusion proteins encoded are vitamin K-dependent protein
gamma-carboxylation enhancers and are useful for optimising the
VKDP. The fusion proteins and recombinant cells expressing them are
useful for alleviating a VKDP associated disease. The fusion
constructs result in the production of fully gamma-carboxylated
mature VKDPs, which are biologically active. The invention
encompasses all combinations of propeptide sequences (modified or
not) and VKDP's. This sequence encodes the signal, propeptide and
mature protein sequence of human factor X.

Sequence 1507 BP; 394 A; 429 C; 446 G; 238 T; 0 other;

Query Match 91.0%; Score 91; DB 21; Length 1507;

Best Local Similarity 94.9%; Pred. No. 3e-22;

Matches 94; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GTCGTACAGAGCCCTGCTCATATGAGAAAAAGAGGTTTCTGTGTGGAACCATTC 61

DB 737 GTCCCTGGCAGGCCCTCTATCATAGAGAAACGAGGGTTCTGTGGAACTATTC 796
 QY 62 TGAGCGAGTTCTACATCTAACGCGACCCACTGTCTCT 100
 DB 797 TGAGCGAGTTCTACATCTAACGCGACCCACTGTCTCT 835

DB 852 TGAGCGAGTTCTACATCTAACGCGACCCACTGTCTCT 890

Search completed: January 15, 2003, 19:50:17
 Job time: 153 secs

RESULT 15

AAH57469

AAH57469 standard; cDNA; 1887 BP.

AC AAH57469;

DT 10-SEP-2001 (first entry)

DE Human liver cell specific cDNA sequence SEQ ID NO:309.

KW Human; tissue specific; diagnosis; brain; heart; skeletal muscle;

KW lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;
 metabolic disease; developmental disease; cytostatic; immunomodulatory;
 neuroprotective; gene therapy; cancer; immunopathology; neuropathology.

OS Homo sapiens.

PN WO200132927-A2.

PD 10-MAY-2001.

PF 02-NOV-2000; 2000WO-US30396.

PR 04-NOV-1999; 99US-0163508.

XX (INCY-) INCYTE GENOMICS INC.

PI Sornasse T, Seilhamer JJ, Watson GA;

DR WPI; 2001-291057/30.

PT New cell and tissue specific polynucleotides useful for diagnosis,
 prognosis or monitoring of treatments for disorders where the gene is
 associated with a cancer, immunopathology or neuropathology -

PS Claim 1; Page 233; 327pp; English.

CC AAH57161 to AAH57576 represent cell and tissue specific polynucleotide
 sequences (I). (I) can have cytosolic, immunomodulatory and
 neuroprotective activities, and can be used in gene therapy. (I) and
 proteins (II) encoded by them are used in high throughput screening
 assays to select DNA molecules, RNA molecules, peptide nucleic acids,
 mimetics, peptides, proteins, agonists, antagonists, antibodies or
 their fragments, immunoglobulins, inhibitors, drug compounds and
 pharmaceutical agents. Expression of (I) in a sample indicates the
 differentiation of embryonic stem cells into a tissue selected from
 brain, heart, kidney, liver, lung, skeletal muscle or pancreatic
 tissues. (I) and (II) are used to produce an expression profile that
 defines a metabolic or developmental process, treatment, condition,
 disease or disorder. The gene profile can be used for diagnosis,
 prognosis or monitoring of treatments and for investigating a
 predisposition to a disorder where the gene is associated with a
 cancer, immunopathology or neuropathology.

CC Sequence 1887 BP; 467 A; 549 C; 544 G; 327 T; 0 other;

Query Match 91.0%; Score 91; DB 22; Length 1887;

Best Local Similarity 94.9%; Pred No. 3.3e-22;
 Matches 94; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GTCTGTACAGCCCTGTCTATCATAGAGAAACGAGGGTTCTGTGTGGAACCATTC 61

DB 792 GTCCCTGGCAGGCCCTCTATCATAGAGAAACGAGGGTTCTGTGTGGAACCATTC 851

QY 62 TGAGCGAGTTCTACATCTAACGCGACCCACTGTCTCT 100

1	92.6	92.6	92.6	725	3	US-09-197-801-12	Sequence 12, App
2	92.6	92.6	92.6	725	4	US-09-551-028-12	Sequence 12, App
3	92.6	92.6	92.6	1126	2	US-08-479-733A-27	Sequence 27, App
4	92.6	92.6	92.6	1126	3	US-08-487-427-27	Sequence 27, App
5	92.6	92.6	92.6	1126	3	US-08-479-727A-27	Sequence 27, App
6	92.6	92.6	92.6	1126	3	US-08-482-359A-27	Sequence 27, App
7	92.6	92.6	92.6	1126	3	PCT-US93-07439-27	Sequence 27, App
8	92.6	92.6	92.6	1404	5	US-09-202-101-15	Sequence 15, App
9	91	91.0	1500	1	US-08-487-037-4	Sequence 4, App	
10	75.2	75.2	591	4	US-09-280-017-138	Sequence 138, App	
11	63.4	63.4	1554	1	US-08-469-486-1	Sequence 1, App	
12	63.4	63.4	1554	2	US-08-469-568-1	Sequence 1, App	
13	34.2	34.2	2038	4	US-09-008-271A-18	Sequence 18, App	
14	34.2	34.2	2079	4	US-09-656-002-1	Sequence 1, App	
15	32	32.0	864	3	US-08-906-769-138	Sequence 138, App	
16	32	32.0	864	3	US-08-906-616-138	Sequence 138, App	
17	32	32.0	864	3	US-08-639-075A-138	Sequence 138, App	
18	32	32.0	864	4	US-09-012-431-138	Sequence 138, App	
19	32	32.0	864	4	US-09-012-692-138	Sequence 138, App	
20	32	32.0	864	4	US-08-906-613-138	Sequence 138, App	
21	30.8	30.8	855	3	US-08-906-769-130	Sequence 130, App	
22	30.8	30.8	855	3	US-08-906-616-130	Sequence 130, App	
23	30.8	30.8	855	3	US-08-639-075A-130	Sequence 130, App	
24	30.8	30.8	855	4	US-09-012-431-130	Sequence 130, App	
25	30.8	30.8	855	4	US-09-012-692-130	Sequence 130, App	
26	30.8	30.8	855	4	US-08-906-613-130	Sequence 130, App	
27	29.4	29.4	758	3	US-08-906-769-126	Sequence 126, App	

45	28	28.0	1389	4	US-09-202-101-16	Sequence 16, App
44	28.8	28.8	258	5	PCT-US05-14442A-52	Sequence 52, App
43	28.8	28.8	258	4	US-08-906-613-52	Sequence 52, App
42	28.8	28.8	258	4	US-09-012-692-52	Sequence 52, App
41	28.8	28.8	258	4	US-09-012-431-52	Sequence 52, App
40	28.8	28.8	258	3	US-08-639-078A-52	Sequence 52, App
39	28.8	28.8	258	3	US-08-485-443B-52	Sequence 52, App
38	28.8	28.8	258	3	US-08-817-795-52	Sequence 52, App
37	28.8	28.8	258	3	US-08-906-616-52	Sequence 52, App
36	28.8	28.8	258	3	US-08-484-211C-52	Sequence 52, App
35	28.8	28.8	258	2	US-08-482-130C-52	Sequence 52, App
34	28.8	28.8	258	2	US-08-485-445D-52	Sequence 52, App
33	28.8	28.8	258	1	US-08-485-445D-52	Sequence 52, App
32	29.4	29.4	758	4	US-08-906-613-126	Sequence 126, App
31	29.4	29.4	758	4	US-09-012-692-126	Sequence 126, App
30	29.4	29.4	758	4	US-09-012-431-126	Sequence 126, App
29	29.4	29.4	758	3	US-08-639-075A-126	Sequence 126, App
28	29.4	29.4	758	3	US-08-906-616-126	Sequence 126, App

ALIGNMENTS

RESULT 1

```

1      Sequence 12, Application US/09197801A
2      Patent No. 6159722
3      GENERAL INFORMATION:
4      APPLICANT: Kopetzki, Erhard
5      APPLICANT: Hopfner, Karl-Peter
6      APPLICANT: Engn, Richard
7      APPLICANT: Bode, Wolfram
8      APPLICANT: Huber, Robert
9      TITLE OF INVENTION: Chimeric Serine Protease
10     FILE REFERENCE: 20119
11     CURRENT APPLICATION NUMBER: US/09/197,801A
12     CURRENT FILING DATE: 1998-11-23
13     NUMBER OF SEQ ID NOS: 15
14     SOFTWARE: PatentIn Ver. 2.0
15     SEQ ID NO 12
16     LENGTH: 72
17     TYPE: DNA
18     ORGANISM: Homo sapiens
19     US-09-197-801-12

```

Query Match

Best Local Similarity 96.08; Pred. No. 4e-25;
Matches 95; Conservat4no 0; Mismatch 4; Indole 0; Cans 0;

2. GTCTGTACAGGCCCTGCTCATCATGAGGAACGAGGGTTCTCTGTGTGGAACCATTC 61

Db 65 GTCCCTGGCAGGCCCTGCTCATCATGAGGAAACGAGGGTTCTGTGTGGAACCATTC 124

62 TGAGCGAGTCTACATCCTAACGGCAGCCGACTGTCTCT 100

DB 125 TGAGCGAGTCTACATCTTACCGGAGCCCACTGTCCT 163

RESULT 2

Sequence 12, Application US/09551028

GENERAL INFORMATION

APPLICANT: Hopfner, Karl-Peter

APPLICANT: Bode, Wolfram
APPLICANT: Hubert, Robert

FILE REFERENCE: 20119

CURRENT FILING DATE: 2000-04-17

1. *Chlorophyll a* (Chl *a*)

PRIOR FILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 12
LENGTH: 725
TYPE: DNA
ORGANISM: Homo sapiens
US-09-551-028-12

Query Match 92.6%; Score 92.6; DB 4; Length 725;
Best Local Similarity 96.0%; Pred. No. 4e-25;
Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTCGTGACAGGCGCCCTGCTCATCATGAGAAACGAGGCTTCTGCTGGAACCATTC 61
DB 65 GTCCTGGCAGGCGCCCTGCTCATCATGAGAAACGAGGCTTCTGCTGGAACCATTC 124
QY 62 TGAGCGAGTTCTACATCTCTAACGCGAGCCCACTGCTCT 100
DB 125 TGAGCGAGTTCTACATCTCTAACGCGAGCCCACTGCTCT 163

RESULT 3

US-08-479-733A-27
Sequence 27, Application US/08479733A
Patent No. 5877289
GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: Edgington, Thomas S.
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Specific Coagulation of Vasculature
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,733A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/273,567
FILING DATE: 11-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:459/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
TELEX: N/A
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1126 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-479-733A-27

Query Match 92.6%; Score 92.6; DB 2; Length 1126;
Best Local Similarity 96.0%; Pred. No. 4.7e-25;
Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 GTCGTGACAGGCGCCCTGCTCATCATGAGAAACGAGGCTTCTGCTGGAACCATTC 61
DB 111 GTCGTGACAGGCGCCCTGCTCATCATGAGAAACGAGGCTTCTGCTGGAACCATTC 61

DB 395 GTCCTGGCAGGCGCCCTGCTCATCATGAGAAACGAGGCTTCTGCTGGAACCATTC 454
QY 62 TGAGCGAGTTCTACATCTCTAACGCGAGCCCACTGCTCT 100
DB 455 TGAGCGAGTTCTACATCTCTAACGCGAGCCCACTGCTCT 493

RESULT 4

US-08-487-427-27
Sequence 27, Application US/08487427
Patent No. 6004555
GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: Edgington, Thomas S.
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Specific Coagulation of Vasculature
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,427
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/273,567
FILING DATE: 11-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:457/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
TELEX: N/A
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1126 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-487-427-27

Query Match 92.6%; Score 92.6; DB 3; Length 1126;
Best Local Similarity 96.0%; Pred. No. 4.7e-25;
Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTCGTGACAGGCGCCCTGCTCATCATGAGAAACGAGGCTTCTGCTGGAACCATTC 61
DB 395 GTCCTGGCAGGCGCCCTGCTCATCATGAGAAACGAGGCTTCTGCTGGAACCATTC 454
QY 62 TGAGCGAGTTCTACATCTCTAACGCGAGCCCACTGCTCT 100
DB 455 TGAGCGAGTTCTACATCTCTAACGCGAGCCCACTGCTCT 493

RESULT 5

US-08-479-727A-27
Sequence 27, Application US/08479727A
Patent No. 6036955
GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Specific Coagulation of Vasculature

```

      FILING DATE: 07-JUN-1995
      CLASSIFICATION: 424
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/273,567
      FILING DATE: 11-JUL-1994
      ATTORNEY/AGENT INFORMATION:
      NAME: Parker, David L.
      REGISTRATION NUMBER: 32,165
      REFERENCE/DOCKET NUMBER: UTSD:433/PAR
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 512/418-3000
      TELEFAX: 512/474-7577
      TELEEX: N/A
      INFORMATION FOR SEQ ID NO: 27:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 1126 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      US-08-482-369A-27

Query Match
Best Local Similarity 92.6%; Score 92.6; DB 3; Length 1126;
Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY 2 GTCCTCAGACAGCCCGTCATCATCATGAGGAAAGAGGCTTCGTGTGGAACCATTC 61
Db 395 GTCCTCAGAGCCCTTCATCATCATGAGGAAAGAGGCTTCGTGTGGAACCATTC 454
QY 62 TGAGCGAGTTCTACATCTTACGCGAGCCCATGCTCT 100
Db 455 TGAGCGAGTTCTACATCTTACGCGAGCCCATGCTCT 493

RESULT 7
PCT-US95-07439-27
Sequence 27, Application PC/TUS9507439
GENERAL INFORMATION:
APPLICANT:
APPLICANT: NAME: BOARD OF REGENTS, THE UNIVERSITY OF
APPLICANT: TEXAS SYSTEM
APPLICANT: STREET: 201 West 7th Street
APPLICANT: CITY: Austin
APPLICANT: STATE: Texas
APPLICANT: COUNTRY: United States of America
APPLICANT: POSTAL CODE: 78701
APPLICANT: TELEPHONE NO: (512)499-4462
APPLICANT: TELEFAX: (512)499-4523
APPLICANT: NAME: THE SCRIPPS RESEARCH INSTITUTE
APPLICANT: STREET: 10666 North Torrey Pines Road
APPLICANT: CITY: LaJolla
APPLICANT: STATE: California
APPLICANT: COUNTRY: United States of America
APPLICANT: POSTAL CODE: 92037
TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: FOR THE SPECIFIC
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII
APPLICATION NUMBER: PCT/US95/07439
FILING DATE: Concurrently herewith
CLASSIFICATION:

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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/273,567
FILING DATE: 11-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTFDA33P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1126 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-07439-27

Query Match 92.6%; Score 92.6; DB 5; Length 1126;
Best Local Similarity 96.0%; Pred. No. 4.7e-25;
Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTCTGTCACAGGCGCTGCTCATCAATGAGGAAAGAGGGTTCTGTGTGGACCATTC 61
||| |
DB 395 GTCCCTGGCAGGCGCTGCTCATCAATGAGGAAAGAGGGTTCTGTGTGGACCATTC 454
||| |
QY 62 TGAGCGAGTTCTACATCCTTAACGGCAGCCCACTGTCTCT 100
||| |
DB 455 TGAGCGAGTTCTACATCCTTAACGGCAGCCCACTGTCTCT 493
||| |

RESULT 8

US-09-202-101-15
Sequence 15, Application US/09202101
Patent No. 6277618
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Recombinant blood-coagulation proteases
NUMBER OF SEQUENCES: 17
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30B (EPO)
CURRENT APPLICATION NUMBER: US/09/202,101
FILING DATE:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-202-101-15

Query Match 92.6%; Score 92.6; DB 4; Length 1404;
Best Local Similarity 96.0%; Pred. No. 5.1e-25;
Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTCTGTCACAGGCGCTGCTCATCAATGAGGAAAGAGGGTTCTGTGTGGACCATTC 61
||| |
DB 683 GTCCCTGGCAGGCGCTGCTCATCAATGAGGAAAGAGGGTTCTGTGTGGACCATTC 742
||| |
QY 62 TGAGCGAGTTCTACATCCTTAACGGCAGCCCACTGTCTCT 100
||| |
DB 743 TGAGCGAGTTCTACATCCTTAACGGCAGCCCACTGTCTCT 781
||| |

RESULT 9
US-08-487-037-4
Sequence 4, Application US/08487037

Patent No. 5795863

GENERAL INFORMATION:
APPLICANT: Wolf, David L.
TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,037

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Adler, Reid G.

REGISTRATION NUMBER: 30,988

REFERENCE/DOCKET NUMBER: 2803-0002.02

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763

TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1500 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-487-037-4

Query Match 94.9%; Score 91; DB 1; Length 1500;

Best Local Similarity 94.9%; Pred. No. 2e-24;

Matches 94; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GTCTGTCACAGGCGCTGCTCATCAATGAGGAAAGAGGGTTCTGTGTGGACCATTC 61
||| |
DB 769 GTCCCTGGCAGGCGCTGCTCATCAATGAGGAAAGAGGGTTCTGTGTGGACCATTC 828
||| |
QY 62 TGAGCGAGTTCTACATCCTTAACGGCAGCCCACTGTCTCT 100
||| |
DB 829 TGAGCGAGTTCTACATCCTTAACGGCAGCCCACTGTCTCT 867
||| |

RESULT 10

US-09-280-116-138/C
Sequence 138, Application US/09280116A
Patent No. 6331427
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24, 05800/17695
CURRENT APPLICATION NUMBER: US/09/280,116A
FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 138
LENGTH: 591
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: trypsin-like serine proteases
NAME/KEY: misc feature
LOCATION: (1)-(591)
OTHER INFORMATION: n = a, t, c or g
US-09-280-116-138

Query Match 75.2%; Score 75.2; DB 4; Length 591;
Best Local Similarity 95.7%; Pred. No. 1.1e-18;
Matches 88; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 6 GTACAGAGCCGCTCATCAATGAGAAACG-AGGCTTTCGTGTCGAAACATCTCTGA 64
DB 499 GTACAGAGCCGCTCATCAATGAGAAACGAGGCTTTCGTGTCGAACTATTCTGA 440

QY 65 GCGAGTTCTACATCCTAACGCGCCACTGT 96
DB 439 GCGAGTTCTACATCCTAACGCGCCACTGT 408

RESULT 11
US-08-469-486-1

; Sequence 1, Application US/08469486
; Patent No. 5739281
; GENERAL INFORMATION:

APPLICANT: Thøgersen, Hans Christian
APPLICANT: Hollet, Thor Ias
APPLICANT: Elzerodt, Michael
TITLE OF INVENTION: Improved method for the refolding of
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
SOFTWARE: #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,486
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bos taurus
FEATURE:
NAME/KEY: CDS
LOCATION: 76..1551
US-08-469-486-1

Query Match 63.4%; Score 63.4; DB 1; Length 1554;
Best Local Similarity 82.0%; Pred. No. 3.6e-14;
Matches 73; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 10 CAGCCCTGCTCATCAATGAGAAACGAGGCTTTCGTGTCGAAACATCTGACGAG 69
DB 817 CAGCTCTGCTCATCAATGAGAAACGAGGATTCGCGGGGACCACTCTGAAACGAG 876

QY 70 TTCTACCTCTCAAGGCGCCACTGCT 98
DB 877 TTCTACCTCTCAAGGCGCCACTGCT 905

RESULT 12
US-08-469-658-1

; Sequence 1, Application US/08469658
; Patent No. 5917018
; GENERAL INFORMATION:

APPLICANT: Thøgersen, Hans Christian
APPLICANT: Hollet, Thor Ias
APPLICANT: Elzerodt, Michael
TITLE OF INVENTION: IMPROVED METHOD FOR THE REPODLING OF
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
SOFTWARE: #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,658
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bos taurus
FEATURE:
NAME/KEY: CDS
LOCATION: 76..1551
US-08-469-658-1

Query Match 63.4%; Score 63.4; DB 2; Length 1554;
Best Local Similarity 82.0%; Pred. No. 3.6e-14;
Matches 73; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 10 CAGCCCTGCTCATCAATGAGAAACGAGGCTTTCGTGTCGAAACATCTGACGAG 69
DB 817 CAGCTCTGCTCATCAATGAGAAACGAGGATTCGCGGGGACCACTCTGAAACGAG 876

REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 2..781
OTHER INFORMATION: /note="At pos. bp 456, change G to
OTHER INFORMATION: K; at pos. bp 504, change A to R. At pos. aa 152 and 168,
OTHER INFORMATION: substitute Xaa."
US-08-906-769-138

Query Match 32.0%; Score 32; DB 3; Length 864;
Best Local Similarity 58.3%; Pred. No. 0.013;
Matches 56; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 3 TCTGTACAGAGCCCTGCTCATCATGAGAAAGAGAGGTTTCTGTGTGAGACCATTC 62
DB 145 TCCGTATCAGATTGCACTGAGAAATCGGACCTAGACCATTTCTGTGTGCTTCATCT 204
QY 63 GAGCGAGTCTACATCCTAAGCGAGCCCACTGTCT 98
DB 205 AACCAACGTTGATTTGTGTGAGCGCTGCACATTCCT 240

Search completed: January 15, 2003, 20:51:15
Job time: 33 secs